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OM nucleic - nucleic search, using sw model

Run on: October 6, 2002, 01:27:03 ; Search time 1893.2 seconds
(without alignments)
3614.503 Million cell updates/sec

Title: US-09-647-780A-3
Perfect score: 327
Sequence: 1 gggcagatcacgcacgg.....tcttcttcacactatgcc 327

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_btg.*

3: gb_in.*

4: gb_ov.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: gb_vl.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

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6	325.4	99.5	2714	6	AX139741	Sequence 3	327 bp	DNA	linear	PAT 07-SEP-2000
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8	323.8	99.0	2076	6	AX146976	Sequence 3	327 bp	DNA	linear	PAT 07-SEP-2000
9	323.8	99.0	2262	6	AX146980	Sequence 3	327 bp	DNA	linear	PAT 07-SEP-2000
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ALIGNMENTS

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DEFINITION	Sequence 3 from Patent WO9553077
ACCESSION	AX014703
VERSION	AX014703.1
KEYWORDS	GI:10040977
SOURCE	human
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE	Novel nep ii membrane metalloprotease and its use for screening
JOURNAL	inhibitors useful in therapy
	Patent: WO 9553077-A 3 21-OCT-1999;
	INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS
	CLAUDE (FR); OUTMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME
	MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
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LOCUS AXI39743 2636 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 3 from Patent EP1069188.
ACCESSION AXI39743
VERSION AXI39743.1 GI:14275325
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Jagerschmidt,A., Agnel,M. and Culouscou,J.M.
TITLE Three neprilysin-like membrane metalloproteinases
JOURNAL Patent: EP 1069188-A 3 17-JAN-2001;
SANOFI-SYNTHELABO (FR)
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Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 301 gagcagctcttcttcacaaactatgcc 327
Db 2063 GAGCAGCTCTTCTTCATCACTATGCC 2089

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LOCUS AXI39745 2663 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 5 from Patent EP1069188.
ACCESSION AXI39745
VERSION AXI39745.1 GI:14275327
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Jagerschmidt,A., Agnel,M. and Culouscou,J.M.
TITLE Three neprilysin-like membrane metalloproteinases
JOURNAL Patent: EP 1069188-A 5 17-JAN-2001;
SANOFI-SYNTHELABO (FR)
FEATURES
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LOCUS
DEFINITION Sequence 14 from Patent WO0047750.
ACCESSION AX033274
VERSION AX033274.1 GI:10280089

KEYWORDS

SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2676)
Boileau, G. and Desgroseillers, L.
AUTHORS
TITLE New metalloproteases of the neprilysin family
JOURNAL Patent: WO 0047750-A 14 17-AUG-2000;
BOILEAU GUY (CA); DESGROSEILLERS LUC (CA); UNIVERSITE DE MONTREAL (CA)

FEATURES

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Best Local Similarity 99.7%; Pred. No. 4.2e-68;
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RESULT 5

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LOCUS
DEFINITION Sequence 1 from Patent EP1069188.
ACCESSION AX139741
VERSION AX139741.1 GI:14275323

KEYWORDS

SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2714)
Jägerschmidt, A., Agnel, M. and Culouscou, J.M.
AUTHORS
TITLE Three neprilysin-like membrane metalloproteinases
JOURNAL Patent: EP 1069188-A 1 17-JAN-2001;
SANOFI-SYNTHELABO (FR)

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RESULT 6
AF336981 AF336981 2784 bp mRNA linear PRI 01-OCT-2001
LOCUS Homo sapiens neprilysin-like metalloproteinase 2 mRNA, complete cds.
DEFINITION AF336981
ACCESSION AF336981
VERSION AF336981.1 GI:15811370
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Bonvouloir, N., Lemieux, N., Crine, P., Boileau, G. and
DesGroselliers, L.
AUTHORS Molecular cloning, tissue distribution, and chromosomal
localization of MME2, a gene coding for a novel human member of
the neutral endopeptidase-24.11 family
JOURNAL DNA Cell Biol. 20 (8), 493-498 (2001)
MEDLINE 21444797
PUBMED 11560781
REFERENCE 2 (bases 1 to 2784)
AUTHORS Bonvouloir, N., Lemieux, N., Crine, P., Boileau, G. and
DesGroselliers, L.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-2001) Biochemistry, University of Montreal, P. O.
Box 6128, Station Centre Ville, Montreal, Quebec H3C 3J7, Canada
FEATURES Location/Qualifiers
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/chromosome="1"
/map="lp36"
65..2377
CDS
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/codon_start=1
/product="neprilysin-like metalloproteinase 2"

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TLRLDANLPWDSCLVEDMVOVLELTOLAKATVPOERHDVIALYHRMGLLELSQ
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RLVLDRIQSQRKDTVRNYRKALPGTWTVEVRWRECVGVYVNSNMENAVGSLVREA
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BASE COUNT 569 a 789 c 841 g 485 t
ORIGIN

Query Match 99.5%; Score 325.4; DB 9; Length 2784;
Best Local Similarity 99.7%; Pred. No. 4.2e-68;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 gggcacgagatcacgcagcgtttgatgacaatggccggaacttcgcagaagaatggcaac 60
DB 1871 GGGCAGAGATCAGCAGCGCTTTGACGACAAATGGCCGGAACCTTCGACAGAAATGGCAAC 1930
QY 61 atgatgattggaggagtaactctccaccagcaacttcggggagcagtcagagtgcatg 120
DB 1931 ATGATGATTGGTGGAGTAACCTTCCACCCAGCAGCTTCGGGGAGCAGTCAGAGTGCAATG 1990
QY 121 atctaccagtacggcaactactcctgggagcagctggcagcagaagaacagcgattc 180
DB 1991 ATCTACCAGTACGGCACTACTCTCGGACCTGGCAGACGAACAGCTGAACGGATTC 2050
QY 181 aacaccttgggaaacattgctgacaacgaggggtggcgaagcctataaagcctac 240
DB 2051 AACACCCCTTGGGNAACATGCTGACACGAGGAGGGTGGCGAAGCCTATAAGGCGCTAC 2110
QY 241 ctcaagtggatggcagaggggtggcaagaccagcagctgcccggcctggatctccaccat 300
DB 2111 CTCAAGTGGATGGCAGAGGTGGCAAGACCAGCAGCTGCCCGGCTGGATCTCACCCAT 2170
QY 301 gacgagctcttcttcacactatgcc 327
DB 2171 GAGCAGCTCTTCTTCATCAACTATGCC 2197

RESULT 7
AX146976 AX146976 2076 bp DNA linear PAT 08-JUN-2001
LOCUS Sequence 1 from Patent WO0136610.
DEFINITION AX146976
ACCESSION AX146976
VERSION AX146976.1 GI:14346247
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 2076)
AUTHORS Deleersnijder, W., Wiegiers, R. and Weske, M.
TITLE Human enzymes of the metalloprotease family
JOURNAL Patent: WO 0136610-A 1 25-MAY-2001.
Solvay Pharmaceuticals B.V. (NL)
FEATURES Location/Qualifiers
source 1. 2076
/organism="Homo sapiens"
/db_xref="taxon:9606"
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CDS
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GAADVNAVYSPNRNOIVFPAGILOPFESKEQOALNFGGIGWVIGHEITHGFDONGR
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BASE COUNT 539 a 649 c 739 g 413 t
ORIGIN

Query Match 99.0%; Score 323.8; DB 6; Length 2340;
Best Local Similarity 99.4%; Pred. No. 1e-67;
Matches 325; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ggcacgagatcacgcagcgtttgatgacaatg---gcggaacttcgacaagaatggc 60
DB 1834 GGCACGAGATCACGCAGCGCTTGACGACAATGGCGGAATTCGACAGAATGGCAAC 1993
QY 61 atgatgattggtggagtaactctccaccagcactctccgggagcagtcagagtgcatg 120
DB 1894 ATGATGGATTGGTGGAGTAACCTCTCCACCAGCACTTCGCGGAGCAGTCAGAGTGCATG 1953
QY 121 attaccagtcagcgaactactctctggacccctggcagacagacagacgtgaacgattc 180
DB 1954 ATCTACAGTACGCAACTACTCTCTGGGACCTGGCAGACAGCAACGAGTGAACGGATTC 2013
QY 181 aacacccctggggaaaaaactctgacacagaggggtgaggcaagccctataaaggccctac 240
DB 2014 AACACCTTGGGGAAAAAATCTGTAACAAGGAGGGGTGCGCAAGCCTATAAGGCGCTAC 2073
QY 241 ctcaagtgtgagcagaggtgagcagacagcagcagtcgcccggcgtgagtcacccat 300
DB 2074 CTCAAGTGTGATGGCAGAGGTGCGCAGGACCAAGCAGCTGCCCGGCTGGATCTCACCCAT 2133
QY 301 ggcagcgtcttcttcatcaactatgcc 327
DB 2134 GAGCAGCTCTCTTCTCATCAACTACGCC 2160

RESULT 10
AX319864
LOCUS AX319864 2232 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 28 from Patent WO0183782.
ACCESSION AX319864
VERSION AX319864.1 GI:17901454
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Plowman,G.D., Whyte,D., Sudarsanam,S., Manning,G., Caenepeel,S. and Payne,V.
TITLE Novel proteases
JOURNAL Patent: WO 0183782-A 28 08-NOV-2001;
Sugen, Inc. (US)
FEATURES
source
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/organism="Homo sapiens"
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BASE COUNT 512 a 620 c 705 g 395 t
ORIGIN

Query Match 95.5%; Score 312.4; DB 6; Length 2232;
Best Local Similarity 98.8%; Pred. No. 5.6e-65;
Matches 326; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 ggcacgagatcacgcagcgtttgatgacaatg---gcggaacttcgacaagaatggc 57
DB 1723 GGCACGAGATCACGCAGCGCTTGACGACAATGGTGGCGGAATTCGACAGAATGGC 1782
QY 58 aacatgatggattggtggagtaactctccaccagcactctccgggagcagtcagagtc 117
DB 1783 AACATGATGGATTGGTGGAGTAACCTCTCCACCAGCACTTCGCGGAGCAGTCAGAGTGC 1842
QY 118 atgatctaccagtcacggcaactactctctgggacactgacagcaagaacagcgtgaacgga 177
DB 1843 ATGATCTACAGTACGCGCACTACTCTCTGGGACCTGCGCAGCAAGCAAGCGTGAACGGA 1902
QY 178 ttcaacacccctggggaaaaaactctgacacgaggggtgaggcaagcctataaaggcc 237
DB 1903 TTCAACACCTTGGGGNAACATCTGTCACACGAGGGGTGCGCAAGCCTATAAGGCC 1962
QY 238 tacctcaagtgtgagcagaggtgagcagacagcagcagtcgcccggcgtgagtcaccc 297
DB 1963 TACCTCAAGTGGATGGCAGAGGTGGCAAGCAGCAGCAGCTGCCCGGCTGGATCTCACC 2022
QY 298 catgagcagcgtcttcttcatcaactatgcc 327
DB 2023 CATGACGAGCTCTCTTCTCATCAACTATGCC 2052

RESULT 11
AF302075
LOCUS AF302075 2583 bp mRNA linear ROD 11-JUN-2001
DEFINITION Mus musculus neprilysin-like peptidase alpha mRNA, complete cds.
ACCESSION AF302075
VERSION AF302075.1 GI:10505359
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2583)
AUTHORS Shirotani,K., Tsubuki,S., Iwata,N., Takaki,Y., Hariyaya,W.,
Wariyama,K., Kiryu-Seo,S., Kiyama,H., Iwata,H., Tomita,T.,
Iwatsubo,T. and Saldo,T.C.
TITLE Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42 Most
Rapidly and Efficiently among Thiorphan- and
Phosphoramidon-sensitive Endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)
JOURNAL 11278416
PUBMED
REFERENCE 2 (bases 1 to 2583)
AUTHORS Shirotani,K. and Saldo,T.C.
TITLE Direct Submission
JOURNAL Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
Science Institute, RIKEN, 2-1 Hirotsawa, Wako-shi, Saitama
351-0198, Japan

FEATURES
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BASE COUNT 565 a 667 c 736 g 515 t
ORIGIN

Query Match 72.6%; Score 237.4; DB 10; Length 2583;
Best Local Similarity 82.9%; Pred. No. 5.8e-47;
Matches 271; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 gggcagagatcacgcagcgtttgatgataaattgctgctraatttgacagacggaac 1806
DB 1747 GGGCAGAGATCACACGCGTGTGATGATAAATGCTGCTRAATTGACAGACGGAAC 1806

QY 61 atgatgattggtggagtaactctccaccagcagcaacttcgggagagtcagagtgcatg 120
DB 1807 ATGTGGAGCTGGTGGAGTAACCTCTCGCCCGGCACATTCACACAGGATCGCAATGATG 1866

QY 121 atctaccagtcacggcaactactctgggacctggcagcagcaagacgtaacgagattc 180
DB 1867 ATCTATCAGTACGGCACTTCTCTTGGGAAGTACGACACACAGATGTGAACGGATTTC 1926

QY 181 aacaccttggggaaaacattgtgacaacggagggtgcggaagcctataagccctac 240
DB 1927 AGTACCTCGGGGAGAACATTCGCGACACGGAGGTGTGCGACAGGATACAAAGCCTTAC 1986

QY 241 ctcaagtgtgagtcagaggtgcaagacagcagcagtcgcccggcctggtatctcaacct 300
DB 1987 CTACGGTGGCTGGCTGATGCGCGCAAGATCAGCAGCTGCGGGGACTGAACCTGACCTAT 2046

QY 301 gacgagctctcttctcaactatgcc 327
DB 2047 GCCCAGCTTTCTTCATCACTATGCC 2073

RESULT 12
AF302076 2652 bp mRNA linear ROD 11-JUN-2001
LOCUS AF302076
DEFINITION Mus musculus neprilysin-like peptidase beta mRNA, complete cds.
ACCESSION AF302076
VERSION AF302076.1 GI:10505361
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2652)
Shirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W.,
Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T.,
Iwatsubo, T. and Saido, T.C.

TITLE Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42 Most
Rapidly and Efficiently among Thiorphan- and
Phosphoramidon-sensitive Endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)

JOURNAL 11278416
PUBMED 2 (bases 1 to 2652)
REFERENCE Shirotani, K. and Saido, T.C.
AUTHORS Direct Submission
TITLE Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
JOURNAL Science Institute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
351-0198, Japan

FEATURES
source Location/Qualifiers
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BASE COUNT 682 a 685 c 755 g 530 t
ORIGIN

Query Match 72.6%; Score 237.4; DB 10; Length 2652;
Best Local Similarity 82.9%; Pred. No. 5.8e-47;
Matches 271; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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DB 1816 GGGCAGAGATCACACGCGTGTGATGATAAATGCTGCTRAATTGACAGACGGAAC 1875

QY 61 atgatgattggtggagtaactctccaccagcagcaacttcgggagagtcagagtgcatg 120
DB 1876 ATGTGGAGCTGGTGGAGTAACCTCTCTTGGGAAGTACGACACAGCAGCTGCAATGCTATG 1935

QY 121 atctaccagtcacggcaactactctgggacctggcagcagcaagacgtaacgagattc 180
DB 1936 ATCTATCAGTACGGCACTTCTCTTGGGAAGTACGACACAGCAGCTGCAATGCTATG 1995

QY 181 aacaccttggggaaaacattgtgacaacggagggtgcggaagcctataagccctac 240
DB 1996 AGTACCTCGGGGAGAACATTCGCGACACGGAGGTGTGCGACAGGATACAAAGCCTTAC 2055

QY 241 ctcaagtgtgagtcagaggtgcaagacagcagcagtcgcccggcctggtatctcaacct 300
DB 2056 CTACGGTGGCTGGCTGATGCGCGCAAGATCAGCAGCTGCGGGGACTGAACCTGACCTAT 2115

QY 301 gacgagctctcttctcaactatgcc 327
DB 2116 GCCCAGCTTTCTTCATCACTATGCC 2142

RESULT 13
AF302077 2694 bp mRNA linear ROD 11-JUN-2001
LOCUS AF302077
DEFINITION Mus musculus neprilysin-like peptidase gamma mRNA, complete cds.
ACCESSION AF302077
VERSION AF302077.1 GI:10505363
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2694)
Shirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W.,
Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T.,
Iwatsubo, T. and Saido, T.C.

TITLE Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42 Most
Rapidly and Efficiently among Thiorphan- and
Phosphoramidon-sensitive Endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)

JOURNAL 11278416
PUBMED 2 (bases 1 to 2694)
REFERENCE Shirotani, K. and Saido, T.C.
AUTHORS Direct Submission
TITLE Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
JOURNAL Science Institute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
351-0198, Japan
FEATURES Location/Qualifiers

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BASE COUNT      686 a 700 c 766 g 542 t
ORIGIN

Query Match      72.6%; Score 237.4; DB 10; Length 2694;
Best Local Similarity 82.9%; Pred. No. 5.8e-47;
Matches 271; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 gggcacgagatcacgcagcggctttgatgacaatggccgggaacttcgacaagaatggcaac 50
D 1858 GGGCAGCAGATCACACACGGCTTTGATGATAATGCTGCTAACTTTGACAGAACGGCAAC 1317
QY 61 atgatgattggtgagtaactctccaccagcactctccggggagcagtcagagtgatg 120
D 1918 ATGCTGGACTGGTGGAGTAACCTTCGCGCCGGCAGCTTCCAAACAGCAGTCGCAATGATG 1977
QY 121 atctaccagtcagcgaactactctctgggaactggcagacagacgaacagtcgaacgattc 180
D 1978 ATCTATCAGTACGGCAACTTCTCTTGGGAACATAGCAGACAAACAGAAATGTGAACGGATT 2037
QY 181 aacaccccttggggaaacattgtgacaacggaggggtggcggaagcctataaagccctac 240
D 2038 AGTACCTCGGGGAGAACATTGCGCGACAGAGGTGTGCGACAGGCATACAGGCTTAC 2097
QY 241 ctcaagtggatggcagaggggtggcaagaccagcagctgcccggcctggtatctcacccat 300
D 2098 CTACGGTGGCTGGCTGATGGCGGCAAGATCAGCGACTGCGGGGACTGACCTGACCTAT 2157
QY 301 gaggcagctcttcttcatacaactatgcc 327
D 2158 GCCCAGCTTTTCTTCATCACTATGCC 2184

RESULT 14
AX033272
LOCUS      2925 bp DNA linear PAT 21-SEP-2000
DEFINITION Sequence 12 from Patent WO0047750.
ACCESSION AX033272
VERSION    AX033272.1 GI:10280087
KEYWORDS   house mouse.
SOURCE     Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 2925)
AUTHORS   Boileau, G. and Desgroseillers, L.
TITLE     New metalloproteases of the neprilysin family
JOURNAL   Patent: WO 0047750-A 12 17-AUG-2000.
BOILEAU GUY (CA); DESGROSEILLERS LUC (CA); UNIVERSITE DE MONTREAL
(CA)

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Location/Qualifiers
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BASE COUNT      710 a 797 c 836 g 582 t
ORIGIN

Query Match      72.6%; Score 237.4; DB 6; Length 2925;
Best Local Similarity 82.9%; Pred. No. 5.8e-47;
Matches 271; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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QY 61 atgatgattggtgagtaactctccaccagcactctccggggagcagtcagagtgatg 120
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QY 121 atctaccagtcagcgaactactctctgggaactggcagacagacgaacagtcgaacgattc 180
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QY 181 aacaccccttggggaaacattgtgacaacggaggggtggcggaagcctataaagccctac 240
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QY 241 ctcaagtggatggcagaggggtggcaagaccagcagctgcccggcctggtatctcacccat 300
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RESULT 15
AF176569
LOCUS      2925 bp mRNA linear ROD 11-MAY-2000
DEFINITION Mus musculus neprilysin-like metalloproteinase 1 (N11) mRNA,
complete cds.
ACCESSION AF176569
VERSION    AF176569.1 GI:7769082
KEYWORDS   house mouse.
SOURCE     Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 2925)
AUTHORS   Ghaddar, G., Ruchon, A.F., Carpentier, M., Marcinkiewicz, M.,
Seidah, N.G., Crine, P., DesGroseillers, L. and Boileau, G.
TITLE     Molecular cloning and biochemical characterization of a new mouse
testis soluble zinc-metalloproteinase of the neprilysin family

```

Biochem. J. 347, 419-429 (2000).
2 (bases 1 to 2925)
Ghaddar, G., Ruchon, A.F., DesGroselliers, L. and Boileau, G.
Direct Submission
Submitted (09-AUG-1999) Biochemistry, University of Montreal, 2900
Edouard Montpetit, Montreal, Que H3T 1J4, Canada.
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710 a 797 c 836 g 582 t

BASE COUNT.
ORIGIN

Query Match	72.6%;	Score 237.4;	DB 10;	Length 2925;
Best Local Similarity	82.9%;	Pred. No. 5.8e-47;		
Matches 271;	Conservative 0;	Mismatches 56;	Indels 0;	Gaps 0;
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QY	121	atctaccagtcacggcaactactctctgggacctggcgcagacgaacgaacgtaacggattc	180	
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QY	181	acacaccttgggaaaaacattgctgacaaacgaggggtgcggcgaagcctataaagccctac	240	
Db	2303	AGTACCCCTCGGGGAGAACATTGCCGACACAGGAGGTGTGCGACAGGCATACAGAGCTTAC	2362	
QY	241	ctcaagtggatggcagaggggtggcaagaccacgacagctgcccgcgctggattctcacccat	300	
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Job time: 3994 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2002, 01:27:58 ; Search time 211.84 Seconds
(without alignments)
2650.260 Million cell updates/sec

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Perfect score: 327
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues 3472872
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	325.4	99.5	2636	AAF59660	Human neprilysin-1
2	325.4	99.5	2663	AAF59661	Human neprilysin-1
3	325.4	99.5	2676	AA63764	CDNA encoding neut
4	325.4	99.5	2714	AAF59659	Human neprilysin-1
5	323.8	99.0	2076	AAF89737	Nucleotide sequenc
6	323.8	99.0	2262	AAF89739	Nucleotide sequenc
7	323.8	99.0	2340	AAF89738	Nucleotide sequenc
8	312.4	95.5	2332	AA597186	Human metalloprote
9	237.4	72.6	2925	AA63763	CDNA encoding neut

10	232.6	71.1	2765	20	AAZ28810	Rat membrane metal
11	203.4	62.2	1124	22	AAH26248	Human secreted pro
12	191	58.4	1226	22	AAH35007	Human colon cancer
13	159.6	48.8	5524	10	AAH90123	DNA encoding human
14	158	48.3	3181	9	AAH90952	Enkephalinase gene
15	158	48.3	3181	15	AAQ62678	Human enkephalinase
16	158	48.3	3181	22	AAH14514	Human neutral endo
17	158	48.3	3181	22	AAH14524	Human neutral endo
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19	158	48.3	3181	22	AAH84083	Human enkephalinase
20	151	46.2	822	13	AAQ22244	Short-form rat enk
21	151	46.2	3243	9	AAH82261	Enkephalinase gene
22	151	46.2	3243	15	AAQ62679	Rat enkephalinase
23	151	46.2	3369	9	AAH81690	Atrial natriuretic
24	138.2	42.3	1986	23	ABL10163	Drosophila melanog
25	128.4	39.3	570	16	AAQ93868	Bovine endothelin
26	128.4	39.3	2129	16	AAQ93874	Bovine endothelin
27	128.4	39.3	2314	16	AAQ93860	Bovine endothelin
28	127.4	39.0	2889	19	AAH96149	Bovine endothelin
29	126.2	38.6	1703	16	AAQ93871	Bovine endothelin
30	120.4	36.8	2440	17	AAH42151	Human endothelin c
31	120.4	36.8	2440	17	AAH31399	Human endothelin c
32	120.4	36.8	2533	16	AAQ93877	Human placental en
33	120.4	36.8	2720	16	AAQ90315	Human ECE gene, H
34	120.4	36.8	2720	16	AAQ93861	Human endothelin c
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36	111.8	34.2	1380	20	AAH34329	Human EST DNA49831
37	111.8	34.2	1380	21	AAH78595	Human EST DNA49831
38	111.8	34.2	1666	22	ABA06579	Human cDNA SEQ ID
39	111.8	34.2	2652	22	AAH80422	DNA encoding poly
40	110.2	33.7	2602	20	AAH34326	Human PRO403 nucle
41	110.2	33.7	2602	21	AAH78592	Human PRO403 nucle
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43	110.2	33.7	3000	21	AAH08402	Human neurotransmi
44	108.6	33.2	7507	21	AAH38169	Metalloendoproteas
45	107	32.7	3291	19	AAV18976	Nucleotide sequenc

ALIGNMENTS

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ID	AAF59660 standard; CDNA; 2636 BP.
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DT	27-APR-2001 (first entry)
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KW	Human; SNEPb; neprilysin-like membrane metalloproteinase;
KW	splice variant; alternative splicing; zinc endopeptidase family;
KW	neuropeptide; peptide hormone; processing; metabolism; vaccine;
KW	drug screening; renal insufficiency; hepatic disease; ischaemia; pain;
KW	hypertension; cancer; inflammation; cardiovascular disease;
KW	neural disease; pancreatic disease; prostatic disease;
KW	respiratory disease; gene therapy; nephrotropic; vasotrophic; analgesic;
KW	cerebroprotective; hypotensive; cytostatic; antiinflammatory;
XX	cardiovascular; hepatotropic; ss.
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PN	EP1059188-A1.
XX	
PD	17-JAN-2001.
XX	
PF	15-JUL-1999; 99EP-0401767.
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PR	15-JUL-1999; 99EP-0401767.
XX	
PA	(SNFI) SANOFI-SYNTHELABO.
XX	

PI Jagerschmidt A, Agnel M, Culouscou J;
XX WPI; 2001-212582/22.
DR P-PSDB; AAB60562.
XX
XX
XX New membrane-associated metalloproteinase SNEPa, SNEPb and SNEPc.
PT polypeptides and polynucleotides, useful for treating e.g. acute and
PT chronic renal insufficiency, pain, stroke; cancer, inflammation, renal
PT and hepatic ischemia
XX
XX
XX Claim 5; Page 30-33; 72pp; English.
PS
XX The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and
CC the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like
CC membrane metalloproteinases and are the products of alternative splicing.
CC The substrate(s) for the SNEP proteins are not as yet known, although
CC the neprilysin family of zinc endopeptidases play key roles in the
CC processing and/or metabolism of neuro-peptides and peptide hormones. SNEP
CC nucleotides may be used as hybridisation probes for cDNA and genomic
CC DNA; to isolate full-length cDNAs and genomic clones encoding SNEPa,
CC SNEPb or SNEPc; to isolate cDNA and genomic clones of SNEP homologues;
CC as research reagents and material for the discovery of treatments and
CC diagnostics for animal and human diseases; and for chromosome
CC identification. The SNEP proteins may be used as immunogens to
CC produce antibodies immunospecific for SNEPa, SNEPb or SNEPc. Such
CC antibodies are used to isolate or identify clones expressing the
CC protein, or to purify the proteins by affinity chromatography.
CC SNEP proteins may also be used in screening for compounds which modulate
CC SNEP endopeptidase activity, and to assess enzymatic cleavage of small
CC molecule substrates in cells, cell-free preparations, chemical libraries
CC and product mixtures. The SNEP proteins (as vaccine compositions),
CC to treat acute and chronic renal insufficiency, renal and hepatic
CC ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as
CC well as cardiovascular, neuronal, pancreatic, prostatic, renal,
CC respiratory or hepatic diseases. They may also be used in modulating
CC peptide activation and/or degradation in the brain or kidney or in
CC another organ, or to diagnose or treat any disorder related to abnormal
CC expression of SNEPa, SNEPb or SNEPc. The present sequence represents
CC cDNA encoding SNEPb.
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XX Sequence 2636 BP; 601 A; 759 C; 813 G; 462 T; 1 other;
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Best Local Similarity 99.7%; Pred. No. 9.1e-81;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1763 gggcagagatcacgcagcgtttgatgacaatggccggaacttcgacagaatggcaac 1822
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Qy 301 gaggcgtctctctcatcaactatgcc 327
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XX AC AAF59661;
XX
XX DT 27-APR-2001 (first entry)
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XX DE Human neprilysin-like membrane metalloproteinase SNEPc cDNA.
XX
XX KW Human; SNEPc; neprilysin-like membrane metalloproteinase;
KW splice variant; alternative splicing; zinc endopeptidase family;
KW neuro-peptide; peptide hormone; processing; metabolism; vaccine;
KW drug screening; renal insufficiency; hepatic disease; ischaemia; pain;
KW hypertension; cancer; inflammation; cardiovascular disease;
KW neuronal disease; pancreatic disease; prostatic disease;
KW respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic;
KW cerebroprotective; hypotensive; cytostatic; anti-inflammatory;
KW cardiovascular; hepatotropic; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1069188-A1.
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XX PD 17-JAN-2001.
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XX PF 15-JUL-1999; 99EP-0401767.
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XX PR 15-JUL-1999; 99EP-0401767.
XX
XX PA (SNFI) SANOFI-SYNTHELABO.
XX
XX PI Jagerschmidt A, Agnel M, Culouscou J;
XX
XX DR WPI; 2001-212582/22.
XX
XX DR P-PSDB; AAB60563.
XX
XX PT New membrane-associated metalloproteinase SNEPa, SNEPb and SNEPc.
XX
XX PT polypeptides and polynucleotides, useful for treating e.g. acute and
XX
XX PT chronic renal insufficiency, pain, stroke, cancer, inflammation, renal
XX
XX PT and hepatic ischemia
XX
XX
XX Claim 5; Page 35-38; 72pp; English.
PS
XX The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and
CC the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like
CC membrane metalloproteinases and are the products of alternative splicing.
CC The substrate(s) for the SNEP proteins are not as yet known, although
CC the neprilysin family of zinc endopeptidases play key roles in the
CC processing and/or metabolism of neuro-peptides and peptide hormones. SNEP
CC nucleotides may be used as hybridisation probes for cDNA and genomic
CC DNA; to isolate full-length cDNAs and genomic clones encoding SNEPa,
CC SNEPb or SNEPc; to isolate cDNA and genomic clones of SNEP homologues;
CC as research reagents and material for the discovery of treatments and
CC diagnostics for animal and human diseases; and for chromosome
CC identification. The SNEP proteins may be used as immunogens to
CC produce antibodies immunospecific for SNEPa, SNEPb or SNEPc. Such
CC antibodies are used to isolate or identify clones expressing the
CC protein, or to purify the proteins by affinity chromatography.
CC SNEP proteins may also be used in screening for compounds which modulate
CC SNEP endopeptidase activity, and to assess enzymatic cleavage of small
CC molecule substrates in cells, cell-free preparations, chemical libraries
CC and product mixtures. The SNEP proteins (as vaccine compositions),
CC to treat acute and chronic renal insufficiency, renal and hepatic
CC ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as
CC well as cardiovascular, neuronal, pancreatic, prostatic, renal,
CC respiratory or hepatic diseases. They may also be used in modulating
CC peptide activation and/or degradation in the brain or kidney or in
CC another organ, or to diagnose or treat any disorder related to abnormal
CC expression of SNEPa, SNEPb or SNEPc. The present sequence represents
CC cDNA encoding SNEPc.
XX
XX

SQ Sequence 2663 BP; 609 A; 769 C; 816 G; 468 T; 1 other;

Query Match 99.5%; Score 325.4; DB 22; Length 2663;
Best Local Similarity 99.7%; Pred. No. 9.1e-81;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 3

AAA63764
ID AAA63764 standard; cDNA; 2676 BP.

XX AC AAA63764;
XX

DT DT
XX 04-DEC-2000 (first entry)

DE DE
XX cDNA: encoding neutral endopeptidase metalloproteinase-like enzyme NL-2.
XX Neprilysin; neutral endopeptidase metalloproteinase-like enzyme;
KW NEP-like enzyme; protein production; protein secretion;
KW neurological disease; Alzheimer's disease; pain; psychiatric disorder;
KW fertility; bone disease; abnormal phosphate metabolism; ss.
XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers
FH 7:2319
CDS /tag= a

FT /product= "neutral endopeptidase metalloproteinase-like
FT enzyme NL-2"

XX W0200047750-A2.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-CA00147.

XX PR 11-FEB-1999; G9CA-2360376

XX PA (UIMO-) UNIV MONTREAL.

XX Desgroseillers L, Boileau G;

XX WPI: 2000-549148/50.

XX P-PSDB; AAB08131.

XX Novel neutral endopeptidase-like metalloproteinase polypeptides and
PT polynucleotides, used to screen for related sequences and enzyme
PT inhibitors, used for the treatment of NL-3 related bone disorders

XX PS Disclosure; Fig 4; 59pp; English.

XX The present sequence encodes a human neutral endopeptidase
CC metalloproteinase-like enzyme, designated NL-2. The specification
CC also describes NL-1 and NL-3. The NL enzymes are used to test for
CC specific inhibitors. The N-terminal region of the enzymes can be used
CC to promote production and secretion of foreign proteins and active
CC biopeptides, using chimeric constructs containing the foreign protein
CC downstream from and in phase with the N-terminal region. The NL enzymes
CC are have been localised to the brain, and may be useful in the
CC treatment of neurological diseases such as Alzheimer's disease, pain,
CC and psychiatric disorders. NL enzymes have also been localised to the
CC testis and ovaries, and may be used to control fertility. They have
CC also been localised to bone, and may be used to treat bone diseases,
CC and abnormal phosphate metabolism related to improper peptide
CC processing by the NL-3 enzyme.

XX Sequence 2676 BP; 608 A; 771 C; 823 G; 474 T; 0 other;

Query Match 99.5%; Score 325.4; DB 21; Length 2676;
Best Local Similarity 99.7%; Pred. No. 9.1e-81;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 atgatgattggtgagtaactctccaccagcaacttcctccgggagcagtcagagtgcatg 120
Db 1873 atgatgattggtgagtaactctccaccagcaacttcctccgggagcagtcagagtgcatg 1932
QY 121 atctaccagtcagcgaactactctctgggacctggcagacgaaactgaaacggattc 180
Db 1933 atctaccagtcagcgaactactctctgggacctggcagacgaaactgaaacggattc 1992
QY 181 aacaccttggggaaaacattgctgacaacgaggggtgaggcaagcctataaagcctac 240
Db 1993 aacaccttggggaaaacattgctgacaacgaggggtgaggcaagcctataaagcctac 2052
QY 241 ctcaagtggatggcagaggtggcaagaccagcagctgcccggcctggatctcacccat 300
Db 2053 ctcaagtggatggcagaggtggcaagaccagcagctgcccggcctggatctcacccat 2112
QY 301 gacgagctctcttcatcaactatgcc 327
Db 2113 gacgagctctcttcatcaactatgcc 2139

RESULT 4

AAF59659
ID AAF59659 standard; cDNA; 2714 BP.

XX AAF59659;

XX 27-APR-2001 (first entry)

XX Human neprilysin-like membrane metalloproteinase SNEPA cDNA.

XX Human; SNEPA; neprilysin-like membrane metalloproteinase;
KW splice variant; alternative splicing; zinc endopeptidase family;
KW neuropeptide; peptide hormone; processing; metabolism; vaccine;
KW drug screening; renal insufficiency; hepatic disease; ischaemia; pain;
KW hypertension; cancer; inflammation; cardiovascular disease;
KW neuronal disease; pancreatic disease; prostatic disease;
KW respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic;
KW cerebroprotective; hypotensive; cytostatic; antiinflammatory;
KW cardiovascular; hepatotropic; ss.

XX Homo sapiens.

XX EP1069188-A1.

xx PD 17-JAN-2001.
 xx PF 15-JUL-1999; 99EP-0401767.
 xx PR 15-JUL-1999; 99EP-0401767.
 xx PA (SNFI) SANOFI-SYNTHELABO.
 xx PI Jagerschmidt A, Agnel M, Culouscou J;
 xx DR WPI; 2001-212582/22.
 xx DR P-PSDB; AAB60561.
 xx
 xx New membrane-associated metalloproteinase SNEPA, SNEPB and SNEPC.
 xx PT polypeptides and polynucleotides, useful for treating e.g. acute and
 xx PT chronic renal insufficiency, pain, stroke, cancer, inflammation, renal
 xx PT and hepatic ischemia
 xx PS Claim 5; Page 25-28; 72pp; English.
 xx
 xx The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and
 xx CC the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like
 xx CC membrane metalloproteinases and are the products of alternative splicing.
 xx CC The substrate(s) for the SNEP proteins are not as yet known, although
 xx CC the neprilysin family of zinc endopeptidases play key roles in the
 xx CC processing and/or metabolism of neuroendocrine and peptide hormones. SNEP
 xx CC nucleotides may be used as hybridisation probes for cDNA and genomic
 xx CC DNA; to isolate full-length cDNAs and genomic clones encoding SNEPa,
 xx CC SNEPb or SNEPc; to isolate cDNA and genomic clones of SNEP homologues;
 xx CC as research reagents and material for the discovery of treatments and
 xx CC diagnostics for animal and human diseases; and for chromosome
 xx CC identification. The SNEP proteins may be used as immunogens to
 xx CC produce antibodies immunospecific for SNEPa, SNEPb or SNEPc. Such
 xx CC antibodies are used to isolate or identify clones expressing the
 xx CC protein, or to purify the proteins by affinity chromatography.
 xx CC SNEP proteins may also be used in screening for compounds which modulate
 xx CC SNEP endopeptidase activity, and to assess enzymatic cleavage of small
 xx CC molecule substrates in cells, cell-free preparations, chemical libraries
 xx CC and product mixtures. The SNEP proteins (as vaccine compositions),
 xx CC SNEP nucleotides, and SNEP activators or inhibitors may be used
 xx CC to treat acute and chronic renal insufficiency, cancer, inflammation, as
 xx CC ischaemia, pain, stroke, hypertensive disease, prostatic, renal,
 xx CC well as cardiovascular, neuronal, pancreatic, cancer, inflammatory, as
 xx CC respiratory or hepatic diseases. They may also be used in modulating
 xx CC peptide activation and/or degradation in the brain or kidney or in
 xx CC another organ, or to diagnose or treat any disorder related to abnormal
 xx CC expression of SNEPa, SNEPb or SNEPc. The present sequence represents
 xx CC cDNA encoding SNEPa.
 xx SQ Sequence 2714 BP; 621 A; 780 C; 836 G; 476 T; 1 other;

Query Match 99.5%; Score 325.4; DB 22; Length 2714;
 Best Local Similarity 99.7%; Pred. No. 9.2e-81;
 Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 gggcagagatcagcagcgggtttgatgacaaatggccgggaacttcgacaaagaatggcaac 60
 Db 1841 gggcagagatcagcagcgggtttgatgacaaatggccgggaacttcgacaaagaatggcaac 1900
 Qy 61 atgatgattggtgagtaacttctccaccagcaacttcgggagcagtcagatgcatg 120
 Db 1901 atgatgattggtgagtaacttctccaccagcaacttcgggagcagtcagatgcatg 1960
 Qy 121 atctaccagtcagcagcaactctctgggacctggcagcagcaacgctgaacgattc 180
 Db 1961 atctaccagtcagcagcaactctctgggacctggcagcagcaacgctgaacgattc 2020
 Qy 181 aacaccttggggaaaacattctgacaaacgaggggttcgggcaagcctataagcctac 240
 Db 2021 aacaccttggggaaaacattctgacaaacgaggggttcgggcaagcctataagcctac 2080

Qy 241 ctcaagtggatggcagaggggtggcgaagaccagcagctgccggcctggatctccaccat 300
 Db 2081 ctcaagtggatggcagaggggtggcgaagaccagcagctgccggcctggatctccaccat 2140
 Qy 301 gagcagctctcttctcattcaactatgcc 327
 Db 2141 gagcagctctcttctcattcaactatgcc 2167
 RESULT 5
 AAF89737
 ID AAF89737 standard; DNA; 2076 BP.
 XX
 AC AAF89737;
 XX
 DT 23-JUL-2001 (first entry)
 XX
 DE Nucleotide sequence of a human metalloprotease enzyme IGS5.
 XX
 KW Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity;
 KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis;
 KW angina pectoris; myocardial infarction; stroke; ulcer; allergy;
 KW benign prostatic hypertrophy; migraine; psychotic disorder;
 KW neurological disorder; autism; multiple sclerosis; Alzheimer's disease;
 KW neurodegenerative disease; sleep disorder; epilepsy; kidney disease;
 KW cardiovascular disease; arteriosclerosis; cerebrovasospasm;
 KW subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
 KW peripheral vascular disease; Raynaud's disease; motility disorder;
 KW gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
 KW inflammation; chemotherapy induced injury; tumour invasion;
 KW immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
 KW severe mental retardation; dyskinesia; Huntington's disease;
 KW Gilles de la Tourette's syndrome; ss.
 XX
 OS Homo sapiens.
 FH
 FT CDS
 FT 1..2076
 FT /*tag= a
 FT /product= "metalloprotease enzyme IGS5"
 PN WO200136610-A1.
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-EPI1532.
 XX
 PR 19-NOV-1999; 99EP-0203862.
 PR 19-NOV-1999; 99NL-1013616.
 PR 31-MAY-2000; 2000EP-0201937.
 PR 31-MAY-2000; 2000NL-1015356.
 XX
 PA (SOLV) SOLVAY PHARM BV.
 PI Deleersnijder W, Wiegiers R, Weske M;
 XX
 DR WPI; 2001-343815/36.
 DR P-PSDB; AAB83840.
 XX
 PT New IGS5 polypeptides useful for treating infections, pain, cancer,
 PT diabetes, obesity, anorexia, bulimia, asthma, schizophrenia,
 PT hypertension, urinary retention and Parkinson's disease
 XX
 PS Claim 11; Page 5-6; 115pp; English.
 XX
 CC The present sequence encodes a human metalloprotease enzyme designated
 CC IGS5. IGS5 polynucleotides and polypeptides are useful for treating
 CC infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma,
 CC Parkinson's disease, acute heart failure, hypotension, hypertension,
 CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
 CC stroke, ulcers, allergies, benign prostatic hypertrophy, migraine,
 CC psychotic and neurological disorders, autism, multiple sclerosis,

CC Alzheimer's disease, and other neurodegenerative diseases, sleep
 CC disorder, epilepsy, cardiovascular diseases, arteriosclerosis,
 CC cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral
 CC infarction, peripheral vascular disease, Raynaud's disease, kidney
 CC diseases, gastrointestinal disorders, motility disorders and conditions
 CC of delayed gastric emptying, post-operative or diabetic gastroparesis,
 CC diarrhoea, inflammations, chemotherapy induced injury, tumour invasion,
 CC immune disorders, arthritis, endotoxin shock, sepsis, complications of
 CC diabetes mellitus, and severe mental retardation and dyskinesias, such
 CC as Huntington's disease or Gilles de la Tourette's syndrome.
 XX
 SQ Sequence 2076 BP; 493 A; 578 C; 636 G; 369 T; 0 other;

Query Match 99.08; Score 323.8; DB 22; Length 2076;
 Best Local Similarity 99.4%; Pred. No. 2.3e-80;
 Matches 325; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gggcagagatcacgcagcgtttgatgacaatggccggaacttcgacaagaatggcaac 60
 DB 1570 gggcagagatcacgcagcgtttgatgacaatggccggaacttcgacaagaatggcaac 1629
 QY 61 atgatgattggtagaataacttccaccagcactccgggagcagtcagatgcatg 120
 DB 1630 atgatgattggtagaataacttccaccagcactccgggagcagtcagatgcatg 1689
 QY 121 atctaccagtcagcgaactactctctgggaactggcagacagaaactgtaacggattc 180
 DB 1690 atctaccagtcagcgaactactctctgggaactggcagacagaaactgtaacggattc 1749
 QY 181 aacacccctgggaaaaattctgcaacagcagggggtggcgaagcctataagcctac 240
 DB 1750 aacacccctgggaaaaattctgcaacagcagggggtggcgaagcctataagcctac 1809
 QY 241 ctcaagtggatggcagagggtggcaagaccagcagctgcccgccgtgattcaccat 300
 DB 1810 ctcaagtggatggcagagggtggcaagaccagcagctgcccgccgtgattcaccat 1869
 QY 301 gaggcagctcttcttcatacaactatgcc 327
 DB 1870 gaggcagctcttcttcatacaactatgcc 1896

RESULT 6

AAF89739
 ID AAF89739 standard; DNA; 2262 BP.

XX AAF89739;

DT 23-JUL-2001 (first entry)

XX Nucleotide sequence of a human metalloprotease enzyme IGS5.

KW Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity;
 KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis;
 KW angina pectoris; myocardial infarction; stroke; ulcer; allergy;
 KW benign prostatic hypertrophy; migraine; psychotic disorder;
 KW neurological disorder; autism; multiple sclerosis; Alzheimer's disease;
 KW neurodegenerative disease; sleep disorder; epilepsy; kidney disease;
 KW cardiovascular disease; arteriosclerosis; cerebrovasospasm;
 KW subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
 KW peripheral vascular disease; Raynaud's disease; motility disorder;
 KW gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
 KW inflammation; chemotherapy induced injury; tumour invasion;
 KW immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
 KW severe mental retardation; dyskinesia; Huntington's disease;
 KW Gilles de la Tourette's syndrome; ss.

XX Homo sapiens.

OS
 XX
 XX
 FH Location/Qualifiers
 FT CDS 1..2262

FT
 XX
 PN
 XX
 XX
 PD
 XX
 PF
 XX
 PR
 PR
 PR
 PR
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 PA
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 PI
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 DR
 DR
 XX
 PT
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 PT
 XX
 PS
 XX
 CC
 CC
 CC
 CC
 CC
 CC
 CC
 CC
 CC
 CC
 CC
 CC
 SQ

W0200136610-A1.

25-MAY-2001.

17-NOV-2000; 2000WO-EP11532.

19-NOV-1999; 99EP-0203862.

31-MAY-2000; 99NL-1013616.

31-MAY-2000; 2000EP-0201937.

31-MAY-2000; 2000NL-1015336.

(SOLV) SOLVAY PHARM BV.

Deleersnijder W, Wiegiers R, Weske M;

WPI; 2001-343815/36.

P-PSDB; AAB83842.

New IGS5 polypeptides useful for treating infections, pain, cancer,
 diabetes, obesity, anorexia, bulimia, asthma, schizophrenia,
 hypertension, urinary retention and Parkinson's disease

Claim 11; Page 8-9; 115pp; English.

The present sequence encodes a human metalloprotease enzyme designated
 IGS5. IGS5 polynucleotides and polypeptides are useful for treating
 infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma,
 Parkinson's disease, acute heart failure, hypotension, hypertension,
 urinary retention, osteoporosis, angina pectoris, myocardial infarction,
 stroke, ulcers, allergies, benign prostatic hypertrophy, migraine,
 psychotic and neurological disorders, autism, multiple sclerosis,
 Alzheimer's disease, and other neurodegenerative diseases, sleep
 disorder, epilepsy, cardiovascular diseases, arteriosclerosis, cerebral
 cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral
 infarction, peripheral vascular disease, Raynaud's disease, kidney
 diseases, gastrointestinal disorders, motility disorders and conditions
 of delayed gastric emptying, post-operative or diabetic gastroparesis,
 diarrhoea, inflammations, chemotherapy induced injury, tumour invasion,
 immune disorders, arthritis, endotoxin shock, sepsis, complications of
 diabetes mellitus, and severe mental retardation and dyskinesias, such
 as Huntington's disease or Gilles de la Tourette's syndrome.

Sequence 2262 BP; 520 A; 628 C; 716 G; 398 T; 0 other;

Query Match 99.08; Score 323.8; DB 22; Length 2262;

Best Local Similarity 99.4%; Pred. No. 2.4e-80;

Matches 325; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gggcagagatcacgcagcgtttgatgacaatggccggaacttcgacaagaatggcaac 60

DB 1756 gggcagagatcacgcagcgtttgatgacaatggccggaacttcgacaagaatggcaac 1815

QY 61 atgatgattggtagaataacttccaccagcactccgggagcagtcagatgcatg 120

DB 1816 atgatgattggtagaataacttccaccagcactccgggagcagtcagatgcatg 1875

QY 121 atctaccagtcagcgaactactctctgggaactggcagacagaaactgtaacggattc 180

DB 1876 atctaccagtcagcgaactactctctgggaactggcagacagaaactgtaacggattc 1935

QY 181 aacacccctgggaaaaattctgcaacagcagggggtggcgaagcctataagcctac 240

DB 1936 aacacccctgggaaaaattctgcaacagcagggggtggcgaagcctataagcctac 1995

QY 241 ctcaagtggatggcagagggtggcaagaccagcagctgcccgccgtgattcaccat 300

DB 1996 ctcaagtggatggcagagggtggcaagaccagcagctgcccgccgtgattcaccat 2055

QY 301 gaggcagctcttcttcatacaactatgcc 327

bb 2056. qaqcagctcttcttcatcaactacgcc 2082

RESULT 7
AAF89738
ID AAF89738 standard; DNA; 2340 BP.

23-JUL-2001 (first entry)

Metalloprotease; IGG5; infection; pain; cancer; diabetes; obesity;
 anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
 hypotension; hypertension; urinary retention; osteoporosis;
 benign prostatic hypertrophy; stroke; ulcer; allergy;
 neurological disorder; autism; multiple sclerosis; Alzheimer's disease;
 neurodegenerative disease; sleep disorder; epilepsy; kidney disease;
 cardiovascular disease; arteriosclerosis; cerebrovasospasm;
 subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
 peripheral vascular disease; Raynaud's disease; motility disorder;
 gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
 inflammation; chemotherapy induced injury; tumour invasion;
 immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
 severe mental retardation; dyskinesia; Huntington's disease;
 Gilles de la Tourette's syndrome; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	1..2340
FFH	/*tag= a
FT	/product= "metallo"
FT	
FT	

WO200136610-A1.

25-MAY-2001.

17-NOV-2000; 2000WO-EP11532.

19-NOV-1999; 99EP-0203862.

PR 19-NOV-1999; 99NL-1013616.

PR 31-MAY-2000; 2000EP-0201937.

PR 31-MAY-2000; 2000NL-1015356.

PA (SOLV) SOLVAY PHARM BV.

PI Deleersnijder W, Wiegers R, Weske M;

DR WPI; 2001-343815/36.

DR P-PSDB; AAB83841.

New IGS5 polypeptides useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease

xx
PS
Claim 11: page 6-7: 115pp: English.

The present sequence encodes a human metalloprotease enzyme designated IGS5. IGS5 polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, psychotic and neurological disorders, autism, multiple sclerosis, Alzheimer's disease, and other neurodegenerative diseases. Sleep disorder, epilepsy, cardiovascular diseases, arteriosclerosis, cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney diseases, gastrointestinal disorders, motility disorders and conditions

```
XX WPI; 2002-041502/05.
DR P-PSDB; AAU72903.
XX
PT Novel protease polypeptide useful for screening for substances that may
PT be used to treat, e.g., cancers, immune-related diseases,
PT cardiovascular disease, migraine, pain, psychotic and inflammatory
PT disorders.
XX
PS Claim 30; Figure 1R-S; 232pp; English.
XX
CC The invention relates to an isolated, enriched, or purified protease
CC polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to
CC screen for substances (S) that may modulate its activity. Administering
CC S (which modulates protease activity in vitro) may be used to treat a
CC disease or disorder selected from cancers (e.g., of tissues, of blood or
CC haematopoietic origin, of the breast, colon, lung, prostate, cervical,
CC brain, ovarian, bladder or kidney), immune-related diseases and
CC disorders, cardiovascular disease, brain or neuronal-associated diseases
CC (e.g., central or peripheral nervous system diseases, migraine, pain,
CC sexual dysfunction, mood disorders, attention disorders, cognition
CC disorders, hypotension, hypertension, psychotic disorders, neurological
CC disorders and dyskinesias), metabolic disorders and inflammatory
CC disorders. (I) may also be useful as a diagnostic tool for a disease or
CC disorder such as those above. AA597159-AA597195 represent human
CC protease coding sequences and primers of the invention.
XX
SQ Sequence 2232 BP; 512 A; 620 C; 705 G; 395 T; 0 other;
XX
Query Match 95.5%; Score 312.4; DB 24; Length 2232;
Best Local Similarity 98.8%; Pred. No. 3 6e-77;
Matches 326; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
XX
QY 1 gggcagagatcacgcacgggtttgatgacaatg---gccggaacttcgacaagaatgac 57
Db 1723 gggcagagatcacgcacgggtttgatgacaatggtggccggaacttcgacaagaatgac 1782
QY 58 aacatgatgattggtgagtaactttccaccagcacttcctccggagcagtcagagtgcc 117
Db 1783 aacatgatgattggtgagtaactttccaccagcacttcctccggagcagtcagagtgcc 1842
QY 118 atgattcaccagtcacgcaactctctctggacacctggcagacgacagacgtaaacgga 177
Db 1843 atgattcaccagtcacgcaactctctctggacacctggcagacgacagacgtaaacgga 1902
QY 178 tcaacacccttggggaaacattgctgacaacgaggggtgcggaagcctataagacc 237
Db 1903 tcaacacccttggggaaacattgctgacaacgaggggtgcggaagcctataagacc 1962
QY 238 tactcgaagtggatggcagaggggtggaaggaacagcagctgcccggcctggatctacc 297
Db 1963 tactcgaagtggatggcagaggggtggaaggaacagcagctgcccggcctggatctacc 2022
QY 298 catgagcagctcttcttcatacaactatgcc 327
Db 2023 catgagcagctcttcttcatacaactatgcc 2052
XX
RESULT 9
AA63763
ID AAA63763 standard; cDNA; 2925 BP.
XX
AC AAA63763;
XX
XX 04-DEC-2000 (first entry)
XX
DE cDNA encoding neutral endopeptidase metalloproteinase-like enzyme, NL-1.
XX
KW Neprilysin; neutral endopeptidase metalloproteinase-like enzyme;
KW NEP-like enzyme; protein production; protein secretion;
KW neurological disease; Alzheimer's disease; pain; psychiatric disorder;
KW fertility; bone disease; abnormal phosphate metabolism; ss.
```

```
XX Mus sp.
XX OS
XX FH Key Location/Qualifiers
XX CDS 332..2629
XX FT /*tag= a
XX FT /product= "neutral endopeptidase metalloproteinase-like
XX enzyme NL-1"
XX
XX PN WO200047750-A2.
XX
XX PD 17-AUG-2000.
XX
XX PF 11-FEB-2000; 2000WO-CA00147.
XX
XX PR 11-FEB-1999; 99CA-2260376.
XX
XX PA (UYMO-) UNIV MONTREAL.
XX
XX PI Desgroselliers L, Bolleau G;
XX
XX WPI; 2000-549148/50.
DR P-PSDB; AAB08130.
XX
XX Novel neutral endopeptidase-like metalloproteinase polypeptides and
XX polynucleotides, used to screen for related sequences and enzyme
XX inhibitors, used for the treatment of NL-3 related bone disorders
XX
XX Disclosure; Fig 3; 59pp; English.
XX
CC The present sequence encodes a murine neutral endopeptidase
CC metalloproteinase-like enzyme, designated NL-1. The specification
CC also describes NL-2 and NL-3. The NL enzymes are used to test for
CC specific inhibitors. The N-terminal region of the enzymes can be used
CC to promote production and secretion of foreign proteins and active
CC bioproteins, using chimeric constructs containing the foreign protein
CC downstream from and in phase with the N-terminal region. The NL enzymes
CC have been localised to the brain, and may be useful in the
CC treatment of neurological diseases such as Alzheimer's disease, pain,
CC and psychiatric disorders. NL enzymes have also been localised to the
CC testis and ovaries, and may be used to control fertility. They have
CC also been localised to bones, and may be used to treat bone diseases,
CC and abnormal phosphate metabolisms related to improper peptide
CC processing by the NL-3 enzyme.
XX
SQ Sequence 2925 BP; 710 A; 797 C; 836 G; 582 T; 0 other;
XX
Query Match 72.6%; Score 237.4; DB 21; Length 2925;
Best Local Similarity 82.9%; Pred. No. 2 8e-56;
Matches 271; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
XX
QY 1 gggcagagatcacgcacgggtttgatgacaatggtggcgaacttcgacaagaatggcaac 60
Db 2123 gggcagagatcacgcacgggtttgatgacaatggtggcgaacttcgacaagaatggcaac 2182
QY 61 atgatggattggtgagtaactttccaccagcacttcctccggagcagtcagagtgatg 120
Db 2183 atgctggactggtgagtaactttccaccagcacttcctccggagcagtcagagtgatg 2242
QY 121 atctaccagtcacgcaactctctctggacacctggcagacgacagacagcagtcagcggatc 180
Db 2243 atctaccagtcacgcaactctctctggacacctggcagacgacagacagcagtcagcggatc 2302
QY 181 aacacccttggggaaacattgctgacaacgaggggtgcggaagcctataagccctac 240
Db 2303 agtacccttggggaaacattgctgacaacgaggggtgcggaagcctataagccctac 2362
QY 241 ctcaagtgatggcagaggggtggaaggaacagcagcagcgtcccgccgctggtatccacct 300
Db 2363 ctcaagtgatggcagaggggtggaaggaacagcagcagcgtcccgccgctggtatccacct 2422
QY 301 gacgagctcttcttcatacaactatgcc 327
```

[illegible]

AAH32943 to AAH37195 and AAG37788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB37789 represent sequences used in the exemplification of the present invention.

N.B. Pages 666 to 682 and page.7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.

Sequence.1226 BP; 270 A; 388 C; 345 G; 213 T; 110 other;

Query Match . 58.4%; Score 191; DB 22; Length 1226;
Best Local Similarity 73.7%; Pred. No. 1.8e-43;

Db	260	atctaccagtacgggaaactactctctggga - ctggcagacgaacagaacgtgagcgtgcc	318
QY	169	-----	168
Db	319	accagcaccaggctcgtgggggtaccggagcccyagccctgagggcgagaggggaag	378
QY	169	-----gtgaacggattcaacaccctt	189
Db	379	taagggccggggctgcgccaaacctgtctctgtgcgcagtgaaaggattcaacaccctt	438
QY	190	ggggaaacattctgcacaacgaggggtgcgcgaagcctataaaggcctaccctcaagtgg	249
Db	439	ggggaaacattctgcacaacgaggggtgcgcgaagcctataaaggcctaccctcaagtgg	498
QY	250	atggcagaagggtggcaaggaccagacagtcgtgccgcctggattctcaccctatgacagctc	309
Db	499	atggcagaagggtggcaaggaccagacgctgcgccgcctggattctcaccctatgacagctc	558
QY	310	ttcttcatacaactatgcc	327
Db	559	ttcttcatacaactatgcc	576

RESULT 13
 ID AAN90123
 ID AAN90123 standard; DNA; 5524 BP.
 XX
 AC
 AAN90123;
 XX
 DT 01-NOV-1989 (first entry)
 XX
 DE DNA encoding human common acute lymphoblastic leukaemia antigen.
 XX
 DNA; human common acute lymphoblastic leukaemia antigen;
 KW analogic; inhibits leukaemia; endopeptidase.
 KW

Db 1983 cagaattattataaaagaatggcgaagaataattacttccctggacttgacctataatcac 2042
 QY 301 gggcagctcttcttcaactatgc 326
 Db 2043 aaacaactattttcttgaacttgc 2068

RESULT 15

AA062678
 ID AA062678 standard; cDNA; 3181 BP.

XX AC AA062678;

XX DT 05-JAN-1995 (first entry)

XX DE Human enkephalinase cDNA.

XX KW Human; enkephalinase; neutral endopeptidase; kidney; intestine; kinin;
 KW kidney brush border neutral proteinase; pituitary; brain; lymph nodes;
 KW -neutrophils; enkephalins; tachykinins; ss.

XX OS Homo sapiens.

XX PH Location/Qualifiers

FT CDS 3..2249

FT /tag= a

FT mat_peptide 21..2246

FT /tag= b

FT allele 1413

FT /tag= c

FT /note= "Nucleotide is A in a different clone
 changing the codon to Thr"

XX PN EP596355-A.

XX PD 11-MAY-1994.

XX PF 23-DEC-1987; 87EP-0117230.

XX PR 24-DEC-1986; 86US-0946566.

XX PR 12-JAN-1987; 87US-0002478.

XX PA (GETH) GENENTECH INC.

XX PI Malfroy-Camine B, Schofield PR;

XX DR WPI: 1994-152785/19.

XX DR P-PSDB; AAR52706.

XX PT Method for assay of enkephalinase using dansylated peptide(s) -
 PT for identification of recombinant enkephalinase

XX PS Disclosure; Fig 1; 61pp; English.

XX CC This sequence encodes human enkephalinase. Enkephalinase is a
 CC neutral endopeptidase or kidney brush border neutral proteinase. It
 CC has been isolated from the kidney, intestine, pituitary, brain and
 CC lymph nodes, and has been detected in many peripheral organs and in
 CC human neutrophils. The distribution of enkephalinase in the brain
 CC closely parallels the distribution of the enkephalins. Mammalian
 CC enkephalinase may be used in the treatment of various pathological
 CC disorders associated with various endogenous peptides, eg.
 CC tachykinins and kinins.

XX SQ Sequence 3181 BP; 1055 A; 582 C; 657 G; 887 T; 0 other;

Query Match

Best Local Similarity 48.3%; Score 158; DB 15; Length 3181;

Matches 221; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 1 gggcagatcacgcagcggctttgatgacaatggcgggaacttcgacaagaatggcaac 60

Db 1743 ggacagaaatcaccccatggcttcgatgacaatggcagaactttaacaaagatggagac 1802
 QY 61 atgatggattggtggagtaacttctccaccacgcaacttccgggagcagtcagatgcatg 120
 Db 1803 ctgcttgactggtggactcaacagtcgtcaagtaactttaaggagcaatcccatgcatg 1862
 QY 121 atctaccagtacgcgaactactctctgggacctggtgacagcaacagaaacgtgaacggattc 180
 Db 1863 gtgtatcagatggaaactttctctgggacctggcaggtggacagcactttaatggaaatt 1922
 QY 181 aacaccttggggaaaaacattgctgacacggaggggtgcggcaagcctataaagcctac 240
 Db 1923 aatacactgggagaaaaacattgctgataatggaggtcttggtaagcatatacagagcctat 1982
 QY 241 ctcaagtggatggcagagggtgccaaggaccagcagctgcccgcctggatctcaccocat 300
 Db 1983 cagaattattataaaagaatggcgaagaaaaattacttctctggacttgacctaaatcac 2042
 QY 301 gagcagctcttcttcaactatgc 326
 Db 2043 aaacaactattttcttgaacttgc 2068

Search completed: October 6, 2002, 02:37:29
 Job time: 4171 sec

Result No.	Query Match	Score	Length	DB	ID	Description
1	39.3	128.4	570	3	US-08-646-273-13	Sequence 13, Appl
2	128.4	39.3	1219	3	US-08-646-273-22	Sequence 22, Appl
3	128.4	39.3	2314	3	US-08-646-273-29	Sequence 29, Appl
4	127.4	39.0	2889	1	US-08-289-112-1	Sequence 1, Appl
5	126.2	38.6	1703	3	US-08-646-273-18	Sequence 18, Appl
6	120.4	36.8	2533	3	US-08-646-273-24	Sequence 24, Appl
7	120.4	36.8	2720	3	US-08-646-273-35	Sequence 35, Appl
8	107	32.7	3291	1	US-08-574-763-1	Sequence 1, Appl
9	103.8	31.7	2560	4	US-09-303-640-1	Sequence 1, Appl
10	37.4	11.4	146	1	US-08-337-268A-54	Sequence 54, Appl
11	37.4	11.4	146	1	US-08-484-570A-54	Sequence 54, Appl
12	37.4	11.4	2576	1	US-08-471-033-35	Sequence 35, Appl
13	37.4	11.4	2576	2	US-08-471-044-35	Sequence 35, Appl
14	37.4	11.4	2576	2	US-08-463-483A-35	Sequence 35, Appl
15	37.4	11.4	2576	2	US-08-471-046A-35	Sequence 35, Appl
16	37.4	11.4	2576	2	US-08-470-566B-35	Sequence 35, Appl
17	37.4	11.4	2576	2	US-08-469-334-35	Sequence 35, Appl
18	37.4	11.4	2576	3	US-09-300-529-35	Sequence 35, Appl
19	37.4	11.4	2655	1	US-08-471-033-17	Sequence 35, Appl
20	37.4	11.4	2655	1	US-08-471-033-26	Sequence 26, Appl
21	37.4	11.4	2655	2	US-08-471-044-17	Sequence 17, Appl
22	37.4	11.4	2655	2	US-08-471-044-26	Sequence 26, Appl
23	37.4	11.4	2655	2	US-08-463-483A-17	Sequence 17, Appl
24	37.4	11.4	2655	2	US-08-463-483A-26	Sequence 26, Appl
25	37.4	11.4	2655	2	US-08-471-046A-17	Sequence 17, Appl
26	37.4	11.4	2655	2	US-08-471-046A-26	Sequence 26, Appl
27	37.4	11.4	2655	2	US-08-470-566B-17	Sequence 17, Appl

QY 121 atctaccagtcagcgaactactctctgagcctgagcagaaacagacagcgtgaacgattc 180
DB 193 GTGGACCACTACGGCAACATATACCTGTGAACGGG-----AGCGGTGAACGGCGG 243
QY 181 aacaccttggggaaacatttctgacaaacagggggtgagcgaacccctataagggctac 240
DB 244 CACACCTCGGGAAACATCGCCGACAAACGGGGGCTCAAGGCGGCTATCGGGCTAC 303
QY 241 ctcaagtgtgagcagaggtgagcagagaccagcagctgcccggcctgagctctcaccat 300
DB 304 CAGAACTGGGTCAAGAAGAAATGGGGTGAACAGACACTGCCACCCTGGGTCTCAACCAAC 363
QY 301 gaggcagctcttcttcaactatgc 326
DB 364 ACCAGCTCTTCTCTGAGTTTGC 389

RESULT 2
US-08-646-273-22
; Sequence 22, Application US/08646273
; Patent No. 6066502
; GENERAL INFORMATION:
; APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,
; APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Heinz.
; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kell & Weinkauff
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.0
; SOFTWARE: Wordperfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,273
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/03706
; FILING DATE: 11-NOV-1994
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2129 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna for mRNA
US-08-646-273-22

Query Match 39.3%; Score 128.4; DB 3; Length 2129;
Best Local Similarity 64.7%; Pred. No. 3e-28;
Matches 211; Conservative 0; Mismatches 106; Indels 9; Gaps 1;

QY 1 gggcagcagatcacgcacgcttggatgacaatggccggaacttcgacaagaatggcaac 60
DB 1632 GGCCACCACTGACTCATGCTTTGATGATCAAGCCGCGAGTACGACAGCAGCAGTGGGAAC 1691
QY 61 atgagtgattggagtaactcttcacccagcacttcgggagcagtgagtgatg 120
DB 1692 CTCGGGCGCTGGTGAAGAATCTCGTCGGTGAAGCGGTCAAGCAGCAGCAGCGGTGCATG 1751
QY 121 atctaccagtcagcgaactactctctgggaacttcgagcagaaacagcagcgtgaacgattc 180
DB 1752 GTGGAGCAGTACGCAACTATAGCTGTAACGGG-----AGCCGGTGAACGGCGG 1802
QY 181 aacaccttgggaaacatttctgacaaacagggggtgagcgaacccctataagggctac 240

DB 1803 CACACCTCGGGAAACATCGCCGACAAACGGGGGCTCAAGCGGCGCTATCGGGCTAC 1862
QY 241 ctcaagtgtgagcagaggtgagcagagaccagcagctgcccggcctgagctcaccat 300
DB 1863 CAGAACTGGGTCAAGAAGAAATGGGGTGAACAGACACTGCCACCCTGGGTCTCAACCAAC 1922
QY 301 gaggcagctcttcttcaactatgc 326
DB 1923 ACCAGCTCTTCTCTGAGTTTGC 1948

RESULT 3
US-08-646-273-29
; Sequence 29, Application US/08646273
; Patent No. 6066502
; GENERAL INFORMATION:
; APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,
; APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Hein
; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kell & Weinkauff
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.0
; SOFTWARE: Wordperfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,273
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/03706
; FILING DATE: 11-NOV-1994
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2314 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna for mRNA
US-08-646-273-29

Query Match 39.3%; Score 128.4; DB 3; Length 2314;
Best Local Similarity 64.7%; Pred. No. 3.1e-28;
Matches 211; Conservative 0; Mismatches 106; Indels 9; Gaps 1;

QY 1 gggcagcagatcacgcacgcttggatgacaatggccggaacttcgacaagaatggcaac 60
DB 1806 GGCCACCACTGACTCATGCTTTGATGATCAAGCCGCGAGAGTACGACAGCAGTGGGAAC 1865
QY 61 atgagtgattggagtaactcttcacccagcacttcgggagcagtgagtgatg 120
DB 1866 CTCGGGCGCTGGTGAAGAATCTCGTCGGTGAAGCGGTCAAGCAGCAGCAGCGGTGCATG 1925
QY 121 atctaccagtcagcgaactactctctgggaacttcgagcagaaacagcagcgtgaacgattc 180
DB 1926 GTGGAGCAGTACGCAACTATAGCTGTAACGGG-----AGCCGGTGAACGGCGG 1976
QY 181 aacaccttgggaaacatttctgacaaacagggggtgagcgaacccctataagggctac 240
DB 1977 CACACCTCGGGAAACATCGCCGACAAACGGGGGCTCAAGGCGGCTATCGGGCTAC 2036
QY 241 ctcaagtgtgagcagaggtgagcagagaccagcagctgcccggcctgagctcaccat 300
DB 2037 CAGAACTGGGTCAAGAAGAAATGGGGTGAACAGACACTGCCACCCTGGGTCTCAACCAAC 2096

US-08-484-570A-54

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, INFORMATION FOR SEQ ID NO: 35:
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, SEQUENCE CHARACTERISTICS:
,     LENGTH: 2576 base pairs
,     TYPE: nucleic acid
,     STRANDEDNESS: single
,     TOPOLOGY: linear
, MOLECULE TYPE: other nucleic acid
, DESCRIPTION: /desc = "Synthetic DNA
, HYPOTHETICAL: NO
, FEATURE:

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; NAME/KEY: CDS
; LOCATION: 9..2564
; OTHER INFORMATION: /note= "Maize optimized sequence
; OTHER INFORMATION: encoding VIPIA(a) with the Bacillus secretion signal removed
; OTHER INFORMATION: contained in PCIB5526"
US-08-471-033-35

Query Match 11.4%; Score 37.4; DB 1; Length 2576;
Best Local Similarity 46.1%; Pred No. 0.094;
Matches 125; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

Qy 36 ccggaacttcgacagaatgcaacatgatgatgggtgagtaacttccaccacgca 95
Db 491 CCCCGAGTTCAACAAGAGGAGGAGGAGGAGTTCCTGGCCAGCCGACGATCAACCT 550
Qy 96 cttccggagcagtcagatgatctaccagtcacgcaactctctgggacctggc 155
Db 551 GTTACCCAGCAGATGAAGCGGAGATCGACGAGACCCGACGAGCGGCGGACGAT 610
Qy 156 agacgaacagacgtgaacggtatcaacaccccttgggaaacattgtgcaacggagg 215
Db 611 CCCCGACCTGTGGGAGGAGAACGGCTACACCATCCAGAACCCGCTGGAAGTGGGA 670
Qy 216 ggtcggaacgctataaggcctaccagtgatggaggggtggcaaggaccagca 275
Db 671 CGACACCTGGCTAGCAGGGCTACACCAAGTTCGTGAGCAACCCCTGGAGAGCCAC 730
Qy 276 gctgcccggcctggatctcaccatgagcag 306
Db 731 CGTGGCGGACCCCTACACCGACTACGAGAG 761

RESULT 13
US-08-471-044-35
; Sequence 35, Application US/08471044
; Patent No. 5840868
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,044
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
```

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; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 - SOLV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9..2564
; OTHER INFORMATION: /note= "Maize optimized sequence
; OTHER INFORMATION: encoding VIPIA(a) with the Bacillus secretion signal remov
; OTHER INFORMATION: contained in PCIB5526"
US-08-471-044-35

Query Match 11.4%; Score 37.4; DB 2; Length 2576;
Best Local Similarity 46.1%; Pred No. 0.094;
Matches 125; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

Qy 36 ccggaacttcgacagaatgcaacatgatgatgggtgagtaacttccaccacgca 95
Db 491 CCCCGAGTTCAACAAGAGGAGGAGGAGTTCCTGGCCAGCCGACGATCAACCT 550
Qy 96 cttccgggagcagtcagatgatctaccagtcacgcaactctctgggacctggc 155
Db 551 GTTACCCAGCAGATGAAGCGGAGATCGACGAGACCCGACGAGCGGCGGACGAT 610
Qy 156 agacgaacagacgtgaacggtatcaacaccccttgggaaacattgtgcaacggagg 215
Db 611 CCCCGACCTGTGGGAGGAGAACGGCTACACCATCCAGAACCCGCTGGAAGTGGGA 670
Qy 216 ggtcgcgcaagcctataaggcctaccagtcacgaggggtggcaaggaccagca 275
Db 671 CGACACCTGGCTAGCAGGGCTACACCAAGTTCGTGAGCAACCCCTGGAGAGCCAC 730
Qy 276 gctgcccggcctggatctcaccatgagcag 306
Db 731 CGTGGCGGACCCCTACACCGACTACGAGAG 761

RESULT 14
US-08-463-483A-35
; Sequence 35, Application US/08463483A
; Patent No. 5849870
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
```

CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,483A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 2576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 9..2564
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
PS-08-463-483A-15

US-08-463-483A-35

Query Match 11.4%; Score 37.4; DB 2; Length 2576;
Best Local Similarity 46.1%; Pred. No. 0.094;
Matches 125; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

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Db	491	CCCCGGATTCAACAAGAGGAGAGCCAGGAGTTCTGTGCCAAGCCAGCAAGATCAACT	550
QY	96	cttcggggagcgtccagatgcatgattccagatcagcgcaactactcctggacctggc	155
Db	551	GTTCACCCAGCAGATGAAGCGCGAGATCGACGAGGACACCGACCGGCGAGCAGCAT	610
QY	156	agacgaacagaacgtgaacggattcaacacctctggggaaaacattgctgacaacggagg	215
Db	611	CCCGGACTCTGGGAGGAGAACGGCTACACCATCCAGAACCGCATCGCCGTCAAGTGGGA	670
QY	216	ggtgcggcagccctataagccctacctaaagtgatggcagaggggtggcaggaccagca	275
Db	671	CGACAGCCTCGGTAGCAAGGGCTACACCAAGTTCGTTGAGCAACCCCTGGAGAGCCAC	730
QY	276	gtgcccggcctggatctcaccctatgacg	306
Db	731	CGTGGGCGACCCCTACACCGACTACGAGAG	761

RESULT 15

US-08-471-046A-35.
Sequence 35, Application US/08471046A
Patent No. 5866326
GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Escruch, Juan J
TITLE OF INVENTION: Method For Isolating Vegetative Insecticidal
TITLE OF INVENTION: Protein Genes
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5866326artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,046A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV8 - SOLV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 2576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 9...2564
OTHER INFORMATION: /note= "Maize optimized sequence
OTHER INFORMATION: encoding VIPIA(a) with the Bacillus secretion signal remov
OTHER INFORMATION: contained in pCIB5526"
US-08-471-046A-35

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Query Match      11.4%; Score 37.4; DB 2; Length 2576;
Best Local Similarity 46.1%; Pred. NO. 0.094;
Matches 125; Conservative 0; Mismatches 146; Indels 0; Gaps 0;
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2002, 00:27:23 ; Search time 1714.12 Seconds
(without alignments)
2574.793 Million cell updates/sec

Title: US-09-647-780A-3
Perfect score: 327
Sequence: 1 gggcagagatcacgcacgg.....tcttcttcacatcatgcc 327

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST:

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
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- 12: gb_gss:*
- 13: em_gss_hum:*
- 14: em_gss_inv:*
- 15: em_gss_pln:*
- 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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3	159.8	48.9	586	10 BI907511	BI907511
4	158	48.3	1144	10 BM459254	BM459254
5	147.8	45.2	610	9 AW465461	AW465461
6	142.6	43.6	926	10 BF968576	BF968576
7	142	43.4	705	9 AI325325	AI325325
8	139.2	42.6	550	10 BE245519	BE245519
9	138.2	42.3	549	10 BE245100	BE245100
10	138.2	42.3	899	9 AW940129	AW940129
11	132.6	40.6	454	9 AI671752	AI671752
12	132.6	40.6	540	10 BF476098	BF476098
13	132	40.4	391	10 BF590024	BF590024
14	131	40.1	476	9 AI702551	AI702551
15	128.2	39.2	443	9 AI566727	AI566727
16	126.4	38.7	563	9 AW086484	AW086484
17	126	38.5	458	9 AI913156	AI913156

18	123.6	37.8	501	10 W89492	W89492
19	123.6	37.8	536	10 BI692693	BI692693
20	120.6	36.9	466	10 WI0214	WI0214
21	120.4	36.8	968	10 BI869244	BI869244
22	120	36.7	517	10 BI326165	BI326165
23	119.8	36.6	660	10 BM491749	BM491749
24	118.8	36.3	423	9 AA895479	AA895479
25	117.4	35.9	479	9 AA450725	AA450725
26	116.8	35.7	485	10 W78610	W78610
27	113.4	34.7	608	10 BI360370	BI360370
28	112.2	34.3	693	10 BE535389	BE535389
29	108	33.0	704	10 BG153322	BG153322
30	107.6	32.9	600	10 BG803768	BG803768
31	107.6	32.9	600	10 BI986454	BI986454
32	107.4	32.8	548	9 AW654249	AW654249
33	107.4	32.8	761	10 BE871194	BE871194
34	106.8	32.7	678	10 BI505516	BI505516
35	106.4	32.5	463	10 W48775	W48775
36	106.2	32.5	249	9 AI874916	AI874916
37	106	32.4	626	10 BJ093321	BJ093321
38	106	32.4	651	10 BJ096397	BJ096397
39	105.6	32.3	592	10 BF044240	BF044240
40	104.2	31.9	530	10 BF562978	BF562978
41	103.8	31.7	889	10 BF663245	BF663245
42	101.2	30.9	665	9 AV329959	AV329959
43	99.6	30.5	905	10 BF124139	BF124139
44	99.2	30.3	357	9 AA026997	AA026997
45	98.6	30.2	822	10 BG283366	BG283366

ALIGNMENTS

RESULT 1
AJ396658 667 bp mRNA linear EST 25-JAN-2001
LOCUS AJ396658 dkfz426 Gallus gallus cDNA clone 27e4r1, mRNA sequence.
DEFINITION AJ396658
ACCESSION AJ396658
VERSION AJ396658.1 GI:7128817
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 667)
AUTHORS Adrakhmanov, I., Lodygin, D., Geroth, P., Arakawa, H., Law, A., Plachy, J., Korn, B. and Buerstedde, J.M.
TITLE A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
JOURNAL Genome Res. 10 (12), 2062-2069 (2000)
MEDLINE 20568495
COMMENT Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
1. 667
/organism="Gallus gallus"
/strain="CB"
/db_xref="taxon:9031"
/clone_lib="27e4r1"
/clone_lib="dkfz426"
/tissue_type="Bursa of Fabricius"
BASE COUNT 219 a 121 c 165 g 160 t 2 others
ORIGIN

Query Match 50.6%, Score 165.6, DB 9; Length 667;
Best Local Similarity 69.0%, Pred. No. 3.7e-33;
Matches 225; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Query Match	48.9%	Score 159.8	DB 10	Length 531	
Best Local Similarity	98.8%	Pred. No. 1.1e-31			
Matches 161	Conservative	0	Mismatches 2	Indels 0	Gaps 0

Qy	165	gaacgtgaacggattcaacaccccttggggaaaacattgtcgaacaacgaggggtgcggca	224
Db	110	GCAGGTGAACGGATTCAACACCCCTTGGGAAAAACATTGCTGCAACGCGAGGGTGGCGCA	169
Qy	225	agcctataaaggccctacctcaagtgtgagcagaggggtggcagaacacgacgctgcccgg	284
Db	170	AGCCTATAAAGCCCTACCTCAAGTGGATGGCAGAGGGTGGCAAGGACCAACGACGACGTGCCCGG	229
Qy	285	cctgatctcaaccatgaacgagctctcttcctcatcaactatgcc	327
Db	230	CCTGGATCTCACCATGAGCAGCTCTTCTTCATCAACTATGCC	272

RESULT	3
BI907511	
LOCUS	BI907511 586 bp mRNA linear EST 16-OCT-2001
DEFINITION	60306563F1 NIH_MGC_l118 Homo sapiens cDNA clone IMAGE:5214609 5', mRNA sequence.
ACCESSION	BI907511
VERSION	BI907511.1
KEYWORDS	EST
SOURCE	GI:16170345
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 586)
TITLE	NIH-MGC http://mgc.nci.nih.gov/
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11539 Row: a Column: 10 High quality sequence stop: 551. Location/Qualifiers 1. 586 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5214609" /clone_lib="NIH_MGC_l118" /tissue_type="leukocyte" /lab_host="DH10B" /note="vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library."
BASE COUNT	132 a 180 c 184 g 90 t
ORIGIN	

Query Match	48.9%	Score 159.8	DB 10	Length 586	
Best Local Similarity	98.8%	Pred. No. 1.2e-31			
Matches 161	Conservative	0	Mismatches 2	Indels 0	Gaps 0

Qy	165	gaacgtgaacggattcaacaccccttggggaaaacattgtcgaacaacgaggggtgcggca	224
Db	156	GCAGGTGAACGGATTCAACACCCCTTGGGAAAAACATTGCTGCAACGCGAGGGTGGCGCA	215

D_b 218 GGACACGAAATCACCCCATGGCTTCGATGACAAATGGCAGAAAT

Oy 1 gggcacagatc acgcacaggcttt gatgacaatgccggaacttcgacagaatggcaac 60
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 218 GGACACGAATCACCCTCGGCTTCGATGACAATGGCAGAAATTTTAAACAGSGATGCAGAC 277

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QY 61 atgattggtggaagtaattctccaccagcagcacttcggggagcagtcagtgatgcatg 120
DB 278 CTGTTGACTGGTGGAGTCAACAGCTCTGCAATAATTTTAAAGACCTTATCCAGTGCATG 337
QY 121 atctacagttacggaactactctctggagcctggcagacgaagaacgctggaacggtatc 180
DB 338 GTGTACAGTATGGGAACCTTCTCTGGGACCTAGCAAAATGGACAGCATCTCAATGGAAAT 397
QY 181 aacaccttggggaacattctgacacgaggggtgcggcagcctataaagcctac 240
DB 398 AATACACTGGGAGAAACATCTGTAATGCTGTATGGCCAAAGCATACAGAGCCTAT 457
QY 241 ctcaagttgagggaggggtggcagagcagcagctgcccggcctggatctcaaccat 300
DB 458 CAAACTATGTATAAAGCATGGTGAAGAAAATTAATCTCTCTGGACCTGACCTAAATCAC 517
QY 301 gacagctctcttcatacaactatgcc 327
DB 518 AGACAACCTGTTCTCTCGAATTTTGC 544

RESULT 6
BF968576 926 bp mRNA linear EST 22-JAN-2001
LOCUS 602271182F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4359141 5'
DEFINITION mRNA sequence.
ACCESSION BF968576
VERSION BF968576.1 GI:12335791
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL 1 (bases 1 to 926)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9998 row: d column: 22
High quality sequence stop: 766.
FEATURES
source
1..926
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4359141"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: adrenal gland; Vector: pCMV-SPORT6; Site: 1.
Noti; Site: 2; SalI; Cloned unidirectionally; oligo-dr
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 286 a 192 c 221 g 227 t
ORIGIN
Query Match 43.6%; Score 142.6; DB 10; Length 926;
Best Local Similarity 67.3%; Pred. No. 4.5e-27;
Matches 216; Conservative 0; Mismatches 104; Indels 1; Gaps 1;

QY 6 cgagatcacgcacggtttgatgacaattggccggaacttcgacaagaatggcaacatgat 65
DB 1 CGAATCACCCATGCTTCGATGACAAATGGGAGAAACCTTAACAAGATGGAGACCTCGT 60

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QY 66 ggattggtggaagtaattctccaccagcagcacttcggggagcagtcagtgatgcatg 125
DB 61 TGACTGTGGGACTCAACAGTCTGCAAGTAACTTTAAGGAGCAATCCCAGTGCATGGTCTGA 120
QY 126 ccagtacgggaactactctctgggacctggcagacgaagaacgctggaacggtatc 185
DB 121 TCAGTATGGAAACATTTCTCTGGGACCTGGCAGGTGGACAGCACCTTAATGGAATTAATAC 180
QY 186 cctgggggaacattctgacacgaggggtgcggcagcctataaagcctaccta 245
DB 181 ACTGGGAGAAACA-TGCTGATATGGAGGCTCTGGTCAAGCATACAGAGCCTATCAGAA 239
QY 246 gtgagtgaggggtggcagagcagcagcagctgcccggcctggatctcaaccatgagca 305
DB 240 TTATATTAAGAAAGTATGGCGAAGAAAATTAATCTCTCTGGACTTGACCTAAATCACAACA 299
QY 306 gctcttcttcatacaactatgc 326
DB 300 ACTATTTTCTTGAACCTTGC 320

RESULT 7
AI325325 705 bp mRNA linear EST 23-DEC-1998
LOCUS ma44c03.y1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
DEFINITION IMAGE:313540 5' similar to gb:J03779 NEPRILYSIN (HUMAN);, mRNA
sequence.
ACCESSION AI325325
VERSION AI325325.1 GI:4059754
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 705)
COMMENT Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:204156
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 459.
FEATURES
source
1..705
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:313540"
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: p7T73D (Pharmacia) with a modified
polylinker; Site:1; Not 1; Site:2; Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGACCGCCGCAATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T73 vector
(Pharmacia). Library went through one round of

```


full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer.

FEATURES

source
Location/Qualifiers
1..549
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="TCBAP2535"
/clone_lib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA"
/sex="male"
/tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/note="Vector: lambda PSB; Site.1: BamHI; Site.2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGGATCGAGCGCCGACGAGAG(T)VN 3'; V-A,C,G; N-A,C,G,T] and then dG tailed. Second strand was primed with a BamHI-dC primer [5'AGAGCTCGGATCCGCGCCGCAATAAATAAT(C) 3']. Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda PSB-vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, Sasaki N, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"
BASE COUNT 183 a 112 c 124 g 129 t 1 others
ORIGIN

Query Match 42.3%; Score 138.2; DB 10; Length 549;
Best Local Similarity 67.4%; Pred. No. 5.2e-26;
Matches 194; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
QY 1 ggcacagatcacgcagcgtttgatgacaaatggccggaacttcgacagaatggcaac 60
DB 249 GGACAGAAATACCCATGCTTCGATGACAAATGGCAGAACTTTAAAGATGGAGAC 308
QY 61 atgatggattggagtaactttccaccagcacttcggggagcagtcagagtgcatg 120
DB 309 CTCGTTGACGTGGGACTCAACAGTCTGCAAGTAACTTTAAGGACCAATCCACGTGCATG 368
QY 121 atctaccagtcaggaactactctctgggaactggcagacgaacagcgtgaacggattc 180
DB 369 GTGTATCAGTATGGAATCTTTCTCGGACCTGGCAGGTGGACAGCACCTTAATGGAATT 428
QY 181 aacaccttgggaaacattctgacacgaggggtgcggaagcctataaaggcctac 240
DB 429 AATACACTGGGAGAAACATCTGCTGATANTGGAGGCTTTGGTCAAGCATACAGAGCCTAT 488
QY 241 ctcaagtggatggcagaggggtggcaagaccagcagctgccggcctg 288
DB 489 CAGATTATATTAAGAATGGGAGAAATAATTACTTCTGGAGCTTG 536

RESULT 10
AW940129/c
LOCUS
DEFINITION AW940129 899 bp mRNA linear EST 23-APR-2001
melanogaster cDNA clone GH03315 3, mRNA sequence.
ACCESSION AW940129.1 GI:8115575
VERSION
KEYWORDS
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 899)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,

TITLE Lewis, S. and Rubin, G.M.
JOURNAL BDGP/HMI Drosophila EST Project
COMMENT Unpublished (2001)
Other_ESTs: GH03315.5prime
Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting poly-T sequence has been removed. hit genomic AE003436: Drosophila melanogaster genomic scaffold 142000013386054 section 20 of 35, complete sequence.: 02/14/2001
Plate: GH.33 row: B column: 3
High quality sequence stop: 819.

FEATURES

source
Location/Qualifiers
1..899
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH03315"
/clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site.1: EcoRI; Site.2: XhoI; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."
BASE COUNT 213 a 223 c 240 g 221 t 2 others
ORIGIN

Query Match 42.3%; Score 138.2; DB 9; Length 899;
Best Local Similarity 66.1%; Pred. No. 6.2e-26;
Matches 216; Conservative 0; Mismatches 108; Indels 3; Gaps 1;
QY 1 ggcacagatcacgcagcgtttgatgacaaatggccggaacttcgacagaatggcaac 60
DB 830 GGCCACAGAGATTACCCAGGATTTCGACGACAAAGGCGAGGAGTTCGACAAAGGAGGCAAC 771
QY 61 atgatggattggagtaactttccaccagcacttcggggagcagtcagagtgcatg 120
DB 770 ATGATGAGTGGTGGAAACAATGCCACCATCGAGGCTTTTCGGAACGCGAGCGTGCCTC 711
QY 121 atctaccagtcaggaactactctctgggaacttcgggaagcagacgaacagcgtgaacggattc 180
DB 710 ATCGATCAGTACTCGCGCTACAAGATTAAACGAGGTGGAC---ATGTTTCATGACGCGGCGG 654
QY 181 aacaccttgggaaacattctgacacgaggggtgcggaagcctataaaggcctac 240
DB 653 ATGACGAGGCGGAGACATCGCGGACAAACGCGGCTCTAAACAGAGCTTTCAGGCGCTAC 594
QY 241 ctcaagtggatggcagaggggtggcaagaccagcagctgccggcctgagctcaccat 300
DB 593 AAGAAATGGGAGACCTTACATGGGCGGAGCAGCAGCTGCCCGGCTTGAACATGATCCAC 534
QY 301 gacagctctcttcatacaactatgcc 327
DB 533 GATCAGCTGTTCTTTCTCACTACGCC 507

RESULT 11
AI671752/c
LOCUS
DEFINITION AI671752 454 bp mRNA linear EST 16-DEC-1999
similar to gb:J03779 NEPRILYSIN (HUMAN);, mRNA sequence.
ACCESSION AI671752.1 GI:4851483
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Search completed: October 6, 2002, 02:00:33
Job time: 5590. sec

tn51a04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2171886 3' similar to gb:J03779 NEPRILYSIN (HUMAN);, mRNA sequence.
ACCESSION AI566727
VERSION AI566727.1 GI:4525179
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo; 1 (bases 1 to 443)
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 518 Std Error: 0.00
Seq primer: -40UP from Gibco
POLYA-No. Location/Qualifiers
1. .443
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2171886"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/notes="Organ: Kidney; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 117 a 100 c 86 g 140 t
ORIGIN

Query Match 39.2%; Score 128.2; DB 9; Length 443;
Best Local Similarity 65.8%; Pred. NO. 2e-23;
Matches 187; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
QY 42 cttcgacaagaatggcaacatgatgattggtgagtaactctccaccagcactccg 101
DB 443 CTTTAAACAAGATGGAGACCTCGTTGACTGGTGACTCAACAGTCTCAAGTAACTTAA 384
QY 102 ggagcagtcagatgcattaccagtcagcgcgaactactcctgggacctggcagacga 161
DB 383 GGAGCAATCCAGTGCATGCTGATCAGTATGGAACCTTTCTCTGGACCTGGCAGGTGG 324
QY 162 acagaacgtgaacgattcaacaccttggggaaacattgctgacaacgaggggtgg 221
DB 323 ACAGCACCTTAATGGAATTAATACCTGGGAGAAACATTTGCTGATTAATGGAGCTCTGG 264
QY 222 gcaagcctataagcctacctcaagtggatggcagaggtggcgaagcagcagctgcc 281
DB 263 TCAGCATACAGAGCCTATCAGAAATATATATAAAGAAATGGGAGAAATATCTTC 204
QY 282 cggcctggatctcaccatgagcagctcttctcatcaactatgc 326
DB 203 TGGACTTGACCTAAATCACAACAACACTATTTTCTTCTGCACTTGC 159


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gb_pat:A44610      + 374.50 773.94 9.6e-35 2129 | A44610 Sequence 22 from Pat
gb_om:BTENDCE     + 374.50 773.19 1.1e-34 2314 | 235306 B.taurus mRNA for en
gb_pat:A44617      + 374.50 773.19 1.1e-34 2314 | A44617 Sequence 29 from Pat
gb_om:S73774      + 374.50 772.11 1.2e-34 2610 | S73774 endothelin convertin
gb_ro:S82653      + 370.50 764.59 3.2e-34 2340 | S82653 endothelin convertin

seq_name: gb_pat:AX146976

seq_documentation_block:
LOCUS      AX146976                      2076 bp      DNA      linear      PAT 08-JUN-2001
DEFINITION Sequence 1 from Patent WO0136610.
ACCESSION  AX146976
VERSION    AX146976.1  GI:14346247
KEYWORDS
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1. (bases 1 to 2076)
AUTHORS   Deleersnijder,W., Wiegers,R. and Weske,M.
TITLE     Human enzymes of the metalloprotease family
JOURNAL   Patent: WO 0136610-A 1 25-MAY-2001;
          Solvay Pharmaceuticals B.V. (NL)
FEATURES   Location/Qualifiers
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Ratio: 5.711      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

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17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
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1670 GGGAGCAGTCAGAGTCGATGATCTACAGTACGGCACTACTCTCTGGGAC 1719
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seq_documentation_block:
LOCUS AX146980 2262 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 5 from Patent WO0136610.
ACCESSION AX146980
VERSION AX146980.1 GI:14346251
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2262)
AUTHORS Deleersnijder, W., Wiegers, R. and Weske, M.
TITLE Human enzymes of the metalloprotease family
JOURNAL Patent: WO 0136610-A 5 25-MAY-2001;
Solvay Pharmaceuticals B.V. (NL)
FEATURES
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ORIGIN

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seq_documentation_block:
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DEFINITION Sequence 3 from Patent WO0136610.
ACCESSION AX146978
VERSION AX146978.1 GI:14346249
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2340)
AUTHORS Deleersnijder, W., Wiegers, R. and Weske, M.
TITLE Human enzymes of the metalloprotease family
JOURNAL Patent: WO 0136610-A 3 25-MAY-2001;
Solvay Pharmaceuticals B.V. (NL)
FEATURES
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LOCUS AX139743 2636 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 3 from Patent EP1069188.
ACCESSION AX139743
VERSION AX139743.1 GI:14275325
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2636)
AUTHORS Jagerschmidt A., Agnel M. and Culouscou J.M.
TITLE Three neprilysin-like membrane metalloproteinases
JOURNAL Patent: EP 1069188-A 3 17-JAN-2001;
SANOFI-SYNTHELABO (FR)
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Location/Qualifiers

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Percent Similarity: 100.000 Percent Identity: 100.000
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LOCUS AX139745 2663 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 5 from Patent EP1069188.
ACCESSION AX139745
VERSION AX139745.1 GI:14275327
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2663)
AUTHORS Jagerschmidt A., Agnel M. and Culouscou J.M.
TITLE Three neprilysin-like membrane metalloproteinases
JOURNAL Patent: EP 1069188-A 5 17-JAN-2001;
SANOFI-SYNTHELABO (FR)
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Location/Qualifiers

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Ratio: 5.711 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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seq_documentation_block:
LOCUS AX033274 2676 bp DNA linear PAT 21-SEP-2000
DEFINITION Sequence 14 from Patent W00047750.
ACCESSION AX033274
VERSION AX033274.1 GI:10280089.

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2676)

AUTHORS Boileau, G. and Desgrosseillers, L.

TITLE New metalloproteases of the neprilysin family
JOURNAL Patent: WO 0047750-A 14 17-AUG-2000;

BOILEAU GUY. (CA) ; DESGROSSEILLERS LUC (CA) ; UNIVERSITE DE MONTREAL
(CA)

FEATURES Location/Qualifiers

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1913 GGGAGCAGTCAGAGTCATGATCTACCACTAGCGCAACTACTCTCTGGGAC 1962

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seq_documentation_block:

LOCUS AX139741 2714 bp DNA linear PAT 30-MAY-2001

DEFINITION Sequence 1 from Patent EP1069188.

ACCESSION AX139741

VERSION AX139741.1 GI:14275323

KEYWORDS

SOURCE human.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2714)
AUTHORS Jagerschmidt,A., Agnel,M. and Culousoou,J.M.
TITLE Three neprilysin-like membrane metalloproteinases
JOURNAL Patent: EP 1069188-A 1 17-JAN-2001;
SANOFI-SYNTHELABO (FR)
FEATURES
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34 rgGluGlnSerGluCysMetIleTyrglnTyrglyAsnTyrsTrpAsp 50
1941 GGGAGCAGTCAGAGTGCATGATCTACCACTACGCAACTACTCTCTGGGAC 1990
51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsnII 67
1991 CTGGCAGACGACAGACAGCGTGAACGGATTCAACACCTTGGGAAAAACAT 2040
2041 TGCTGCAACGAGGAGGGTGGCGAAGCCTATAGGCCTACTCTCAAGTGA 2090
84 eLaAGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
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101 GluGlnLeuPhePheIleAsnTyralaGlnValTrpCysGly 114
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2141 GAGCAGCTCTTCTTCATCAACTATGCCCGAGGTGTGTGCGGG 2182
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seq_documentation_block:
LOCUS AF336981 2784 bp mRNA linear PRI 01-OCT-2001
DEFINITION Homo sapiens neprilysin-like metalloproteinase 2 mRNA, complete cds.
ACCESSION AF336981
VERSION AF336981.1 GI:15811370
KEYWORDS
SOURCE
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2784)
AUTHORS Bonvouloir,N., Lemieux,N., Crine,P., Boileau,G. and
DesGroselliers,L.
Molecular cloning, tissue distribution, and chromosomal
localization of MMEL2, a gene coding for a novel human member of
the neutral endopeptidase-24.11 family
JOURNAL DNA Cell Biol. 20 (8), 493-498 (2001)
MEDLINE 21444797
PUBMED 11560781
REFERENCE 2 (bases 1 to 2784)
AUTHORS Bonvouloir,N., Lemieux,N., Crine,P., Boileau,G. and
DesGroselliers,L.
Direct Submision
TITLE Submitted (15-JAN-2001) Biochemistry, University of Montreal, P. O.
JOURNAL Box 6128, Station Centre Ville, Montreal, Quebec H3C 3J7, Canada
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67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
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2071 TGCTGACAACGGAGGGTGGCGAAGCTATAAGGCCTACCTCAAGTGA 2120

84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
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2121 TGGCAGAGGGTGGCAAGACAGCAGCTGCCCGCTGGATCTCACCCAT 2170

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seq_documentation_block:
LOCUS AX319864 2232 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 28 from Patent WO0183782.
ACCESSION AX319864
VERSION AX319864.1 GI:17901454
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Playman,G.D., Whyte,D., Sudarsanam,S., Manning,G., Caenepeel,S. and
Payne,V.
TITLE Novel proteases
JOURNAL Patent: WO 0183782-A 28 08-NOV-2001;
Sugen, Inc. (US).
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Location/Qualifiers
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16 pLysAsnGlyAsnMetMetAspTrpTrpSerAsnPheserThrGlnHisP 33
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33 heargGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrp 49
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83 rpMetAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThr 99
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1973 CGATGGCAGAGGGTGGCAAGACAGCAGCTGCCCGCTGGATCTCACCC 2022

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seq_name: gb_pat:AX014703
seq_documentation_block:
LOCUS AX014703 327 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 3 from Patent WO9953077.
ACCESSION AX014703
VERSION AX014703.1 GI:10040977
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 327)
AUTHORS Schwartz,J.C., Gros,C., Ouimet,T., Rose,C., Bonhomme,M.C. and
Facchinetti,P.
TITLE Novel nep ii membrane metalloprotease and its use for screening
inhibitors useful in therapy
JOURNAL Patent: WO 9953077-A 3 21-OCT-1999;
INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS
CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME
MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
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51 GAATGGCAACATGATGATTGGTGGAGTAACCTTCCACCCAGCACTTCC 100

34 rgGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpasp 50
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seq_name: gb_ro:AF302075

seq_documentation_block:

LOCUS AF302075 2583 bp mRNA linear ROD 11-JUN-2001

DEFINITION Mus musculus neprilysin-like peptidase alpha mRNA, complete cds.

ACCESSION AF302075

VERSION AF302075.1 GI:10505359

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2583)

AUTHORS Shirotsani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W.,
Maruyama, K., Kiriya-See, S., Kiyama, H., Iwata, H., Tomita, T.,
Iwatsubo, T. and Saido, T.C.

TITLE Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42. Most
Rapidly and Efficiently among Thiorphan- and
Phosphoramidon-sensitive Endopeptidases

J. Biol. Chem. 276 (24), 21895-21901 (2001).

11278416

REFERENCE 2 (bases 1 to 2583)

AUTHORS Shirotsani, K. and Saido, T.C.

Direct Submission

TITLE Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
Science Institute, RIKEN, 2-1 Hirotsawa, Wako-shi, Saitama

351-0198, Japan

11278416

FEATURES

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BASE COUNT 665 a 667 c 736 g 515 t

ORIGIN

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17 sAsnGlyAsnMetMetAspTrrPrrSerAsnPheSerThrGlnHisPheA 34
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1797 GAACGGCAACATCTGGACTGGTGGAGTAACCTTCTCGCCCGGCACTTC 1846
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34 rgGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50
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1847 AACAGCAGTCGCAATGCAATGATCTATCAGTACGGCAACTTCTCTTGGAA 1896
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101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGly 114
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seq_name: gb_ro:AF302076

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LOCUS AF302076 2652 bp mRNA linear ROD 11-JUN-2001

DEFINITION Mus musculus neprilysin-like peptidase beta mRNA, complete cds.

ACCESSION AF302076

VERSION AF302076.1 GI:10505361

KEYWORDS house mouse.

SOURCE Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2652)

AUTHORS Shirotsani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W.,
Maruyama, K., Kiriya-See, S., Kiyama, H., Iwata, H., Tomita, T.,
Iwatsubo, T. and Saido, T.C.

TITLE Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42. Most
Rapidly and Efficiently among Thiorphan- and
Phosphoramidon-sensitive Endopeptidases

J. Biol. Chem. 276 (24), 21895-21901 (2001)

11278416

REFERENCE 2 (bases 1 to 2652)

AUTHORS Shirotsani, K. and Saido, T.C.

Direct Submission

TITLE Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
Science Institute, RIKEN, 2-1 Hirotsawa, Wako-shi, Saitama

351-0198, Japan

11278416

FEATURES

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Ratio: 5.142 Gaps: 0

Percent Similarity: 99.123 Percent Identity: 85.088

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Quality: 581.00 Length: 114
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51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsn 67

1966 CTAGCAGACACACAGATGTGAACGGATTGACACCTCCGCGGGAGAACAT 2015

67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84

2016 TGCCGACACGGAGGTGTGCGACAGGCATACAAAGCTTACCTACGGTGGC 2065

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2066 TGGCTGATGGCGGCAAGATCAGCGACTGCGGGACTGACCTGACCTAT 2115

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seq_documentation_block:

LOCUS AF302077 2694 bp mRNA linear ROD 11-JUN-2001
DEFINITION Mus musculus neprilysin-like peptidase gamma mRNA, complete cds.

ACCESSION AF302077

VERSION AF302077.1 GI:10505363

KEYWORDS

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2694)

REFERENCE

AUTHORS

Shirota, K., Tsukuba, S., Iwata, N., Takaki, Y., Harigaya, W.,
Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T.,
Iwatsubo, T. and Saido, T.C.

TITLE

Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42 Most
Rapidly and Efficiently among Rhiorphan- and
Phosphoramidon-sensitive Endopeptidases

JOURNAL

PUBMED

11278416

REFERENCE

AUTHORS

Shirota, K. and Saido, T.C.

TITLE

Direct Submission

JOURNAL

Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
Science Institute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
351-0198, Japan

FEATURES

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GYPDILEDNNKHLDEEYSLTFEDLYFENGLNKNNAORSLKILREKVDONLHIGAAVNVN

GAAVNAYSPNRNIVFPAGILOPPFFSKDQPSLNFQIGWIGHEITHGDDNGRNFDDKNG

NFDKNGMLDWSNFSARHFQOQSCMIYOYGNFSEWELADQNVNFGFTIGENIADNGGVQ

RAYKYLRLWADGKQORLGLNLTAYALFFINAYAOVWCGSYRPEFAVOSIKTDV

HSPLKYRYLGLSLQNLPGFSEAFHCPRGSPHMKRCRIW"

BASE COUNT 686 a 700 c 766 g 542 t
ORIGIN

alignment_scores:

Quality: 581.00 Length: 114

Ratio: 5.142 Gaps: 0

Percent Similarity: 99.123 Percent Identity: 85.088

alignment_block:

US-09-647-780A-4 x AF302077

Align seg 1/1 to: AF302077 from: 1 to: 2694

1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAsp 17

1858 GGCACGAGATCACACACGGCTTTCATGATATGCTGCTAACTTTGACAA 1907

17 sAsnGlyAsnMetMetAspTTPTrpSerAsnPheSerThrGlnHisPheA 34

1908 GAACGGCAACATGCTGGACTGGTGGAGTAACTTCTCGGCCCGGCACTTCC 1957

34 rGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50

1958 AACAGCAGTCGCAATGATGATCATCATGACGACGCACTTCTCTGGGAA 2007

51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsn 67

2008 CTAGCAGACACACAGATGTGAACGGATTGACCTCCCTCGGGAGAACAT 2057

67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84

2058 TGCCGACACAGGAGGTGTGCGACAGGCATACAAAGCTTACCTACGGTGGC 2107

84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100

2108 TGGCTGATGGCGGCAAGATCAGCGACTGCGGGAGTGAACCTGACCTAT 2157

101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGly 114

2158 GCCCAGCTTTTCTTCATCACTATGCCAGGTGTGGTGGG 2199

seq_name: gb_pat:AX033272

seq_documentation_block:

LOCUS AX033272

2925 bp

DNA

linear

PAT 21-SEP-2000


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|||||
2123 GGGCAGGATCACACGGCTTTGATGATATGGTCGTAACCTTTGACAA 2172
17 sasnglyAsnMetMetAspTrpSerAsnPheSerThrGlnHisPheA 34
|||||
2173 GAAACGGCAACATGCTGGACTGCTGGAGTAACCTCTCGGCCCGGCACTTCC 2222
34 rgGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpasp 50
:::::
2223 AACACAGTCGCAATGCATGATCTATCAGTAGCGCAACTTCTTTGGGAA 2272
51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsnI1 67
|||||
2273 CTAGCAGACAACCAAGATGTGACGGATTACGTACCTCGGGAGAGACAT 2322
67 ealaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
|||||
2323 TGCCGACACACGGAGGTGTCCGACAGGCATACAAAGGCTTACCTACGGTGGC 2372
84 etAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
:::::
2373 TGGCTGATGGCGGCAAGATCAGCGACTCCCGGACTGAACCTGACCTAT 2422
101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysgly 114
|||||
2423 GCCCAGCTTTTCTTCATCAACTATGCCCAGGTGTGGTGGG 2464
```


CC cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral
CC infarction, peripheral vascular disease, Raynaud's disease, kidney
CC diseases, gastrointestinal disorders, motility disorders and conditions
CC of delayed gastric emptying, post-operative or diabetic gastroparesis,
CC diarrhoea, inflammations, chemotherapy induced injury, tumour invasion,
CC immune disorders, arthritis, endotoxin shock, sepsis, complications of
CC diabetes mellitus, and severe mental retardation and dyskinesias, such
CC as Huntington's disease or Gilles de la Tourette's syndrome.
XX
SQ Sequence 2076 BP; 493 A; 578 C; 636 G; 369 T; 0 other;

alignment_scores:
Quality: 651.00 Length: 114
Ratio: 5.711 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-647-780A-4 x AAF89737

Align seg 1/1 to: AAF89737 from: 1 to: 2076

1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPhAspLy 17
1570 GGGCAGGATCACCGCGCTTTCACGACATGGCGGAATTCGACAA 1619
17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPhSerThrGlnHisPheA 34
1620 GAATGGCAACATGATGGATGTGGAGTAACCTTCCACCCAGCACCTCC 1669
34 rGluGlnSerGluCysMetIleTyTGlnTyGlyAsnTySerTrpAsp 50
1670 GGGCAGGATCACCGCGCTTTCACGACATGGCGGAATTCGACAA 1719
51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsn 67
1720 CTGGCAGAGCAACAGACGCTGAACGATTCACACCCCTTTGGGAAACAT 1769
67 eAlaAspAsnGlyValArgGlnAlaTyrlsAlaTyrlsLeuLysTrpM 84
1770 TGCTGACACAGGAGGGTGGCGCAAGCCCTATAGGCTTACCTCAAGTGA 1819
84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
1820 TGGCAGAGGTCGCAAGGACAGCAGCTCCCGGCTGTGATCACCCT 1869
101 GluGlnLeuPhePheIleAsnTyrlsAlaGlnValTrpCysGly 114
1870 GAGCAGCTCTTCTTCATCACTACGCCAGGCTGTGTGCGGG 1911
seq_name: /SIDS1/9cgcdata/geneseq/geneseq-emb1/NR2001A.DAT:AAF89739
seq_documentation_block:
ID AAF89739 standard; DNA; 2262 BP.
XX
AC AAF89739;
XX
XX
XX 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of a human metalloprotease enzyme IGS5.
XX
KW Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity;
KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
KW hypotension; hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; stroke; ulcer; allergy;
KW benign prostatic hypertrophy; migraine; psychotic disorder;
KW neurological disorder; autism; multiple sclerosis; Alzheimer's disease;
KW neurodegenerative disease; sleep disorder; epilepsy; kidney disease;
KW cardiovascular disease; arteriosclerosis; cerebrovasospasm;
KW subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
KW peripheral vascular disease; Raynaud's disease; motility disorder;
KW gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
KW inflammation; chemotherapy induced injury; tumour invasion;

KW immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
KW severe mental retardation; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2262
FT /tag= a
FT /product= "metalloprotease enzyme IGS5"

XX WO200136610-A1.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000WO-EPI1532.

XX 19-NOV-1999; 99EP-0203862.

XX 19-NOV-1999; 99NL-1013616.

XX 31-MAY-2000; 2000EP-0201937.

XX 31-MAY-2000; 2000NL-1015356.

XX (SOLV) SOLVAY PHARM BV.

XX Deleersnijder W, Wiegers R, Weske M;

XX WPI: 2001-343815/36.

XX P-PSDB: AAB83842.

XX New IGS5 polypeptides useful for treating infections, pain, cancer,
XX diabetes, obesity, anorexia, bulimia, asthma, schizophrenia,
XX hypertension, urinary retention and Parkinson's disease

XX Claim 11; Page 8-9; 115pp; English.

XX The present sequence encodes a human metalloprotease enzyme designated
XX IGS5. IGS5 polynucleotides and polypeptides are useful for treating
XX infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma,
XX Parkinson's disease, acute heart failure, hypotension, hypertension,
XX urinary retention, osteoporosis, angina pectoris, myocardial infarction,
XX stroke, ulcers, allergies, benign prostatic hypertrophy, migraine,
XX psychotic and neurological disorders, autism, multiple sclerosis,
XX Alzheimer's disease, and other neurodegenerative diseases. Sleep
XX cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, kidney
XX infarction, peripheral vascular disease, Raynaud's disease, cerebral
XX diseases, gastrointestinal disorders, motility disorders and conditions
XX of delayed gastric emptying, post-operative or diabetic gastroparesis,
XX diarrhoea, inflammations, chemotherapy induced injury, tumour invasion,
XX immune disorders, arthritis, endotoxin shock, sepsis, complications of
XX diabetes mellitus, and severe mental retardation and dyskinesias, such
XX as Huntington's disease or Gilles de la Tourette's syndrome.

SQ Sequence 2262 BP; 520 A; 628 C; 716 G; 398 T; 0 other;

alignment_scores:

Quality: 651.00 Length: 114
Ratio: 5.711 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-647-780A-4 x AAF89739

Align seg 1/1 to: AAF89739 from: 1 to: 2262

1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPhAspLy 17
1756 GGGCAGGATCACCGCGCTTTCACGACATGGCGGAATTCGACAA 1805
17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPhSerThrGlnHisPheA 34
1806 GAATGGCAACATGATGGATGTGGTGAAGTAACCTTCTCCACCCAGCACCTCC 1855

34 rgGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSertTrpasp 50
|||||
1856 GGGAGCAGTCAGAGTCATGATCTACAGTACGCAACTACTCTCGGAC 1905

51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsn11 67
|||||
1906 CTGGCAGACGACAGACAGCTGACGAGGATCAACACCTTGGGGAAACAT 1955

67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
|||||
1956 TGCTGACACGAGGGGTGGCGCAAGCTATAGGCTTACCTCAAGTGA 2005

84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
|||||
2006 TGGCAGAGGGTGGCAAGGACGACAGCTGCCCGCTGGATCTCACCCAT 2055

101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGly 114
|||||
2056 GAGCAGCTCTTCTTCATCACTACGCCCCAGGTGTGGTGGGG 2097

seq_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAF89738

seq_documentation_block:

ID AAF89738 standard; DNA: 2340 BP.

XX AC AAF89738;

XX DT 23-JUL-2001 (first entry)

XX DE Nucleotide sequence of a human metalloprotease enzyme IG55.

KW Metalloprotease; IG55; infection; pain; cancer; diabetes; obesity;
KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
KW hypertension; hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; stroke; ulcer; allergy;
KW benign prostatic hypertrophy; migraine; psychotic disorder;
KW neurological disorder; autism; multiple sclerosis; Alzheimer's disease;
KW neurodegenerative disease; sleep disorder; epilepsy; kidney disease;
KW cardiovascular disease; arteriosclerosis; cerebrovasospasm;
KW subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
KW peripheral vascular disease; Raynaud's disease; motility disorder;
KW gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
KW inflammation; chemotherapy induced injury; tumour invasion;
KW immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
KW severe mental retardation; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 1..2340

XX FT /*tag= a

XX FT /product= "metalloprotease enzyme IG55"

XX PN WO200136610-A1.

XX PD 25-MAY-2001.

XX PF 17-NOV-2000; 2000WO-EP11532.

XX PR 19-NOV-1999; 99EP-0203862.

XX PR 19-NOV-1999; 99NL-1013616.

XX PR 31-MAY-2000; 2000EP-0201937.

XX PR 31-MAY-2000; 2000NL-1015356.

XX PA (SOLV) SOLVAY PHARM BV.

XX PI Deleersnijder W, Wiegiers R, Weske M;

XX DR WPI; 2001-343815/36.

XX DR P-PSDB; RAB83841.

XX

PT New IG55 polypeptides useful for treating infections, pain, cancer,
PT diabetes, obesity, anorexia, bulimia, asthma, schizophrenia;
PT hypertension, urinary retention and Parkinson's disease
XX
XX Claim 11; Page 6-7; 115pp; English.
XX
CC The present sequence encodes a human metalloprotease enzyme designated
CC IG55. IG55 polynucleotides and polypeptides are useful for treating
CC infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma,
CC Parkinson's disease, acute heart failure, hypotension, hypertension,
CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC stroke, ulcers, allergies, benign prostatic hypertrophy, migraine,
CC psychotic and neurological disorders, autism, multiple sclerosis,
CC Alzheimer's disease, and other neurodegenerative diseases, sleep
CC disorder, epilepsy, cardiovascular diseases, arteriosclerosis,
CC cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral
CC infarction, peripheral vascular disease, Raynaud's disease, kidney
CC diseases, gastrointestinal disorders, motility disorders and conditions
CC of delayed gastric emptying, post-operative or diabetic gastroparesis,
CC diarrhoea, inflammations, chemotherapy induced injury, tumour invasion,
CC immune disorders, arthritis, endotoxin shock, sepsis, complications of
CC diabetes mellitus, and severe mental retardation and dyskinesias, such
CC as Huntington's disease or Gilles de la Tourette's syndrome.

XX SQ Sequence 2340 BP; 539 A; 649 C; 739 G; 413 T; 0 other;

alignment_scores:
Quality: 651.00 Length: 114
Ratio: 5.711 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-647-780A-4 x AAF89738

Align seg 1/1 to: AAF89738 from: 1 to: 2340

1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAspLY 17
|||||
1834 GGGCAGAGATCAGCAGCGCTTTCAGCAGCANTGGCGGAATTCGACAA 1883

17 SASnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
|||||
1884 GAATGGCAACATGATGATGGTGGAGTAACTTCTCCACCCAGCAGCTTCC 1933

34' rgGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSertTrpasp 50
|||||
1934 GGGAGCAGTCAGAGTCATGATCTACAGTACGCGCAACTACTCTCTGGGAC 1983

51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsn11 67
|||||
1984 CTGGCAGACGACAGACAGCTGACGAGGATCAACACCTTGGGGAAACAT 2033

67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
|||||
2034 TGCTGACACGAGGGGTGGCGCAAGCTATAGGCTTACCTCAAGTGA 2083

84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
|||||
2084 TGGCAGAGGGTGGCAAGGACGACAGCTGCCCGCTGGATCTCACCCAT 2133

101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGly 114
|||||
2134 GAGCAGCTCTTCTTCATCACTACGCCCCAGGTGTGGTGGGG 2175

seq_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAF59660

seq_documentation_block:

ID AAF59660 standard; cDNA: 2636 BP.

XX XX

XX AC AAF59660;

XX DT 27-APR-2001 (first entry)

xx DE Human neprilysin-like membrane metalloproteinase SNEPb cDNA.

xx KW Human; SNEPb; neprilysin-like membrane metalloproteinase;

xx KW splice variant; alternative splicing; zinc endopeptidase family;

xx KW neuropeptide; peptide hormone; processing; metabolism; vaccine;

xx KW drug screening; renal insufficiency; hepatic disease; ischaemia; pain;

xx KW hypertension; cancer; inflammation; cardiovascular disease;

xx KW neuronal disease; pancreatic disease; prostatic disease;

xx KW respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic;

xx KW cerebroprotective; hypotensive; cytostatic; antiinflammatory;

xx KW cardiovascular; hepatotropic; ss.

OS Homo sapiens.

xx KW

xx KW EPI069188-AL.

xx PD 17-JAN-2001.

xx KW

xx KW 15-JUL-1999; 99EP-0401767.

xx KW

xx KW 15-JUL-1999; 99EP-0401767.

xx KW (SNFI) SANOFI-SYNTHELABO.

xx KW

xx KW Jagerschmidt A, Agnel M, Culouscou J;

xx KW

xx KW WPI: 2001-212582/22.

xx KW P-PSDB: AAB60562.

xx KW

xx KW New membrane-associated metalloproteinase SNEPA, SNEPb and SNEPC

xx KW polypeptides and polynucleotides, useful for treating e.g. acute and

xx KW chronic renal insufficiency, pain, stroke, cancer, inflammation, renal

xx KW and hepatic ischemia

xx KW

xx KW Claim 5; Page 30-33; 72pp; English.

xx KW

xx KW The invention relates to the human SNEPA, SNEPb and SNEPC proteins, and

xx KW the cDNAs encoding them. SNEPA, SNEPb and SNEPC are neprilysin-like

xx KW membrane metalloproteinases and are the products of alternative splicing.

xx KW The substrate(s) for the SNEP proteins are not as yet known, although

xx KW the neprilysin family of zinc endopeptidases play key roles in the

xx KW processing and/or metabolism of neuropeptides and peptide hormones. SNEP

xx KW nucleotides may be used as hybridisation probes for cDNA and genomic

xx KW DNA; to isolate full-length cDNAs and genomic clones encoding SNEPA,

xx KW SNEPb or SNEPC; to isolate cDNA and genomic clones of SNEP homologues;

xx KW as research reagents and material for the discovery of treatments and

xx KW diagnostics for animal and human diseases; and for chromosome

xx KW identification. The SNEP proteins may be used as immunogens to

xx KW produce antibodies immunospecific for SNEPA, SNEPb or SNEPC. Such

xx KW antibodies are used to isolate or identify clones expressing the

xx KW protein, or to purify the proteins by affinity chromatography.

xx KW SNEP proteins may also be used in screening for compounds which modulate

xx KW SNEP endopeptidase activity, and to assess enzymatic cleavage of small

xx KW molecule substrates in cells, cell-free preparations, chemical libraries

xx KW and product mixtures. The SNEP proteins (as vaccine compositions),

xx KW SNEP nucleotides, and SNEP activators or inhibitors may be used

xx KW to treat acute and chronic renal insufficiency, cancer, inflammation, as

xx KW ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as

xx KW well as cardiovascular, neuronal, pancreatic, prostatic, renal,

xx KW respiratory or hepatic diseases. They may also be used in modulating

xx KW peptide activation and/or degradation in the brain or kidney or in

xx KW another organ, or to diagnose or treat any disorder related to abnormal

xx KW expression of SNEPA, SNEPb or SNEPC. The present sequence represents

xx KW cDNA encoding SNEPb.

xx KW

xx KW Sequence 2636 BP; 601 A; 759 C; 813 G; 462 T; 1 other;

alignment_scores:

Quality: 651.00 Length: 114

Ratio: 5.711 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-647-780A-4 x AAF59660.

Align seg 1/1 to: AAF59660 from: 1 to: 2636

1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAspLy 17

1763 GGGCAGGAGATCAGCAGCGCTTTGACGACAAATGGCGGAATTCGACAA 1812

17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34

1813 GAATGCAACATGATGGATTGGTGGAGTAACCTTCTCCACCCAGCAGCTTC 1862

34 rGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50

1863 GGGAGCAGTCAGAGTCATGATCTACCACTAGCGCAACTACTCTCTGGGAC 1912

51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsnI 67

1913 CTGGCAGACGACAGACAGACGTCAGACGATTCACACCCCTTGGGGAACAT 1962

67 eAlaAspAsnGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84

1963 TGTGACAAACGGGGGTGGCGCAAGCCTATAAGGCTACCTCAAGTGA 2012

84 eTAlaGluGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100

2013 TGGCAGAGGTGGCAAGGACCGACGCTGCCCGGCTGGATCTCACCCT 2062

101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGly 114

2063 GAGCAGCTCTTCTTCATCACTATGCCAGGTGCTGGTGGCGG 2104

seq_name: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT-AAF59661

seq_documentation_block:

ID AAF59661 standard; cDNA; 2663 BP.

XX AC AAF59661;

XX DT 27-APR-2001 (first entry)

XX DE Human neprilysin-like membrane metalloproteinase SNEPc cDNA.

XX KW Human; SNEPc; neprilysin-like membrane metalloproteinase;

XX KW splice variant; alternative splicing; zinc endopeptidase family;

XX KW neuropeptide; peptide hormone; processing; metabolism; vaccine;

XX KW drug screening; renal insufficiency; hepatic disease; ischaemia; pain;

XX KW hypertension; cancer; inflammation; cardiovascular disease;

XX KW neuronal disease; pancreatic disease; prostatic disease;

XX KW respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic;

XX KW cerebroprotective; hypotensive; cytostatic; antiinflammatory;

XX KW cardiovascular; hepatotropic; ss.

OS Homo sapiens.

xx KW

xx KW EPI069188-AL.

xx KW

xx KW 17-JAN-2001.

xx KW

xx KW 15-JUL-1999; 99EP-0401767.

xx KW

xx KW 15-JUL-1999; 99EP-0401767.

xx KW (SNFI) SANOFI-SYNTHELABO.

xx KW

xx KW Jagerschmidt A, Agnel M, Culouscou J;

xx KW

xx KW WPI: 2001-212582/22.

xx KW P-PSDB: AAB60563.

xx KW

xx KW New membrane-associated metalloproteinase SNEPA, SNEPb and SNEPC

polypeptides and polynucleotides, useful for treating e.g. acute and chronic renal insufficiency, pain, stroke, cancer, inflammation, renal and hepatic ischemia.

Claim 5; Page 35-38; 72pp; English.

The invention relates to the human SNEPB, SNEPB and SNEPC proteins, and the cDNAs encoding them. SNEPB, SNEPB and SNEPC are neprilysin-like membrane metalloproteinases and are the products of alternative splicing. The substrate(s) for the SNEP proteins are not as yet known, although the neprilysin family of zinc endopeptidases play key roles in the processing and/or metabolism of neuropeptides and peptide hormones. SNEP nucleotides may be used as hybridisation probes for cDNA and genomic DNA; to isolate full-length cDNAs and genomic clones encoding SNEPB, SNEPB or SNEPC; to isolate cDNA and genomic clones of SNEP homologues; as research reagents and material for the discovery of treatments and diagnostics for animal and human diseases; and for chromosome identification. The SNEP proteins may be used as immunogens to produce antibodies immunospecific for SNEPB, SNEPB or SNEPC. Such antibodies are used to isolate or identify clones expressing the protein, or to purify the proteins by affinity chromatography. SNEP proteins may also be used in screening for compounds which modulate SNEP endopeptidase activity, and to assess enzymatic cleavage of small molecule substrates in cells, cell-free preparations, chemical libraries and product mixtures. The SNEP proteins (as vaccine compositions), SNEP nucleotides, and SNEP activators or inhibitors may be used to treat acute and chronic renal insufficiency, renal and hepatic ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as well as cardiovascular, neuronal, pancreatic, prostatic, renal, respiratory or hepatic diseases; they may also be used in modulating peptide activation and/or degradation in the brain or kidney or in another organ, or to diagnose or treat any disorder related to abnormal expression of SNEPB, SNEPB or SNEPC. The present sequence represents cDNA encoding SNEPB.

Sequence 2663 BP; 609 A; 769 C; 816 G; 468 T; 1 other:

alignment_scores: Quality: 651.00 Length: 114
Ratio: 5.711 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-647-780A-4 x AAF59661

Align seg 1/1 to: AAF59661 from: 1 to: 2663

1 GlyHisGluIleThrHisGlyPheAspAspAsnGlyArgAsnPheAspLY 17
|||||
1790 GGGCAGCAGATACAGCAGCGCTTGGACGACATGGCGGACATTCGACAA 1839

17 sasnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
|||||
1840 GAATGCCAACATGATGATTGGTGGAGTAACTTCTCCACCCAGCACTTC 1889

34 rgGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50
|||||
1890 GGGCAGAGTCAGAGTCAGTATCTACAGTACGCACTACTCTCTGGGAC 1939

51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsnII 67
|||||
1940 CTGGCAGACGACAGACGATGACGATTTCAACACCTTGGGGAACAT 1989

67 eAlaAspAsnGlyGlyValArgGlnAlaTyrIleValTyrLeuLYSTpm 84
|||||
1990 TGGTGAACACGAGGGGTGGCGCAACCTTAAGGCTTCACTCACTGGA 2039

84 eAlaGluGlyGlyAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
|||||
2040 TGGCAGAGGGTGGCAGGACAGCAGCTGCCGCGCTGGATCTTCACCCAT 2089

101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGly. 114

|||||
2090 GAGCAGCTCTCTTCATCACTATGCCAGCTGTGGTGGG 2131

seq_name: /SDSI/gcdata/geneseq/geneseq-emb1/NA2000.DAT:AAA63764

seq_documentation_block:
ID AAA63764 standard; CDNA; 2676 BP.
XX
AC AAA63764;
XX
DT 04-DEC-2000 (first entry)
XX
DE cDNA encoding neutral endopeptidase metalloproteinase-like enzyme NL-2.
XX
KW Neprilysin; neutral endopeptidase metalloproteinase-like enzyme;
KW NEP-like enzyme; protein production; protein secretion;
KW neurological disease; Alzheimer's disease; pain; psychiatric disorder;
KW fertility; bone disease; abnormal phosphate metabolism; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..2319
FT /*tag= a
FT /product= "neutral endopeptidase metalloproteinase-like
FT enzyme NL-2"

WO200047750-A2.
17-AUG-2000.
11-FEB-2000; 2000WO-CA00147.
11-FEB-1999; 99CA-2260376.
(UYMO-) UNIV MONTREAL.
Desgroseillers L, Boileau G;
WPI; 2000-549148/50.
P-PSDB; AAB08131.
Novel neutral endopeptidase-like metalloproteinase polypeptides and
polynucleotides, used to screen for related sequences and enzyme
inhibitors, used for the treatment of NL-3 related bone disorders
Disclosure: Fig 4; 59pp; English.
The present sequence encodes a human neutral endopeptidase
metalloproteinase-like enzyme, designated NL-2. The specification
also describes NL-1 and NL-3. The NL enzymes are used to test for
specific inhibitors. The N-terminal region of the enzymes can be used
to promote production and secretion of foreign proteins and active
biopeptides, using chimeric constructs containing the foreign protein
downstream from and in phase with the N-terminal region. The NL enzymes
are have been localised to the brain, and may be useful in the
treatment of neurological diseases such as Alzheimer's disease, pain,
and psychiatric disorders. NL enzymes have also been localised to the
testis and ovaries, and may be used to control fertility. They have
also been localised to bones, and may be used to treat bone diseases,
and abnormal phosphate metabolisms related to improper peptide
processing by the NL-3 enzyme.

Sequence 2676 BP; 608 A; 771 C; 823 G; 474 T; 0 other:

alignment_scores: Quality: 651.00 Length: 114
Ratio: 5.711 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-647-780A-4 x AAA63764

Align seg 1/1 to: AAA63764 from: 1 to: 2676

```
1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAspLy 17
|||||
1813 GGGCAGAGATCAGCAGCGCTTTGACGAAATGGCGGAACATTCGACAA 1862
|||||
17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
|||||
1863 GAATGGCAACATGATGGATGGTGGAGTAACTTCTCCACCACGACTTCC 1912
|||||
34 rGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50
|||||
1913 GGGAGCAGTCAGAGTCATGATCTACCGAGTACGCAACTACTCTCTGGGAC 1962
|||||
51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsnII 67
|||||
1963 CTGGCAGAGCAGACAGACGCTGACGAGTTCACACACCTTTGGGGAAACAT 2012
|||||
67 eAlaAspAsnGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
|||||
2013 TGCTGACACGGAGGGGTGGGCAACCTATAGCGCTACCTCAATGGGA 2062
|||||
84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
|||||
2063 TGGCAGAGGTGGCAAGGACAGCAGCTGCCGCGCTGGATCTCACCCAT 2112
|||||
101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGly 114
|||||
2113 GAGCAGCTCTTCTTCATCAACTATGCCAGGTGTGTGCGGG 2154
|||||
```

seq_name: /SID1/3cgdata/geneseq/geneseq-emb1/NA2001A.DAT.AAF59659

seq_documentation_block:

ID AAF59659 standard; cDNA; 2714 BP.

XX AAF59659;

27-APR-2001 (first entry)

XX Human neprilysin-like membrane metalloproteinase SNEPA cDNA.

DE Human; SNEPA; neprilysin-like membrane metalloproteinase;
KW splice variant; alternative splicing; zinc endopeptidase family;
KW neurotensin; peptide hormone; processing; metabolism; vaccine;
KW drug screening; renal insufficiency; hepatic disease; ischaemia; pain;
KW hypertension; cancer; inflammation; cardiovascular disease;
KW neuronal disease; pancreatic disease; prostatic disease;
KW respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic;
KW cerebroprotective; hypotensive; cytostatic; antiinflammatory;
KW cardiovascular; hepatotropic; ss.

XX Homo sapiens.

XX EP1069188-A1.

XX 17-JAN-2001.

XX 15-JUL-1999; 99EP-0401767.

XX 15-JUL-1999; 99EP-0401767.

XX (SNFI) SANOFI-SYNTHELABO.

XX Jagerschmidt A, Agnel M, Culouscou J;

XX WPI; 2001-212582/22.

XX P-PSDB; AAB60561.

XX New membrane-associated metalloproteinase SNEPA, SNEPB and SNEPC
PT polypeptides and polynucleotides, useful for treating e.g. acute and
PT chronic renal insufficiency, pain, stroke, cancer, inflammation, renal
PT and hepatic ischemia

XX PS

XX Claim 5; Page 25-28; 72pp; English.

XX The invention relates to the human SNEPA, SNEPB and SNEPC proteins, and
CC the cDNAs encoding them. SNEPA, SNEPB and SNEPC are neprilysin-like
CC membrane metalloproteinases and are the products of alternative splicing.
CC The substrate(s) for the SNEP proteins are not as yet known, although
CC the neprilysin family of zinc endopeptidases play key roles in the
CC processing and/or metabolism of neurotensin and peptide hormones. SNEP
CC nucleotides may be used as hybridisation probes for cDNA and genomic
CC DNA; to isolate full-length cDNAs and genomic clones encoding SNEPA,
CC SNEPB or SNEPC; to isolate cDNA and genomic clones of SNEP homologues;
CC as research reagents and material for the discovery of treatments and
CC diagnostics for animal and human diseases; and for chromosome
CC identification. The SNEP proteins may be used as immunogens to
CC produce antibodies immunospecific for SNEPA, SNEPB or SNEPC. Such
CC antibodies are used to isolate or identify clones expressing the
CC protein, or to purify the proteins by affinity chromatography.
CC SNEP proteins may also be used in screening for compounds which modulate
CC SNEP endopeptidase activity, and to assess enzymatic cleavage of small
CC molecule substrates in cells, cell-free preparations, chemical libraries
CC and product mixtures. The SNEP proteins or inhibitors may be used
CC SNEP nucleotides, and SNEP activators or inhibitors may be used
CC to treat acute and chronic renal insufficiency, cancer, inflammation, as
CC ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as
CC well as cardiovascular, neuronal, pancreatic, prostatic, renal,
CC respiratory or hepatic diseases. They may also be used in modulating
CC peptide activation and/or degradation in the brain or kidney or in
CC another organ, or to diagnose or treat any disorder related to abnormal
CC expression of SNEPA, SNEPB or SNEPC. The present sequence represents
CC cDNA encoding SNEPA.

XX SQ Sequence 2714 BP; 621 A; 780 C; 836 G; 476 T; 1 other;

alignment_scores:

Quality: 651.00 Length: 114

Ratio: 5.711 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-647-780A-4 x AAF59659

Align seg 1/1 to: AAF59659 from: 1 to: 2714

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1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAspLy 17
|||||
1841 GGGCAGAGATCAGCAGCGCTTTGACGAAATGGCGGAACATTCGACAA 1890
|||||
17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
|||||
1891 GAATGGCAACATGATGGATGGTGGAGTAACTTCTCCACCACGACTTCC 1940
|||||
34 rGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50
|||||
1941 GGGAGCAGTCAGAGTCATGATCTACCGAGTACGCAACTACTCTCTGGGAC 1990
|||||
51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsnII 67
|||||
1991 CTGGCAGACGACAGACGCTGACGAGTTCACACACCTTTGGGGAAACAT 2040
|||||
67 eAlaAspAsnGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
|||||
2041 TGCTGACACGGAGGGGTGGGCAACCTATAGCGCTACCTCAATGGGA 2090
|||||
84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
|||||
2091 TGGCAGAGGTGGCAAGGACAGCAGCTGCCGCGCTGGATCTCACCCAT 2140
|||||
101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGly 114
|||||
2141 GAGCAGCTCTTCTTCATCAACTATGCCAGGTGTGTGCGGG 2182
|||||
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seq_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:AAS97186

seq_documentation_block:

ID AAS97186 standard; cDNA; 2232 BP.

XX AC AAS97186;

XX 26-FEB-2002 (first entry)

XX Human metalloprotease partial DNA sequence #15.

XX Human; protease; PCR primer; cytostatic; immunomodulator; cardiant;
 KW vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser;
 KW hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic;
 KW anorectic; antiinflammatory; aspartyl protease; cysteine protease;
 KW metalloprotease; serine protease; cancer; haematopoietic; breast; colon;
 KW lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain;
 KW immune-related disease; cardiovascular disease; neuronal disease;
 KW migraine; sexual dysfunction; mood disorder; attention disorder;
 KW cognition disorder; hypotension; hypertension; psychotic disorder;
 KW dyskinesia; metabolic disorder; inflammatory disorder; ss.

XX Homo sapiens.

XX WO200183782-A2.

XX 08-NOV-2001.

XX 04-MAY-2001; 2001WO-US14431.

XX 04-MAY-2000; 2000US-201879P.

XX (SUGE-) SUGEN INC.

XX Plowman CD, Whyte D, Sudarsanam S, Manning G, Caenepeel S;

XX Payne V;

XX WPI; 2002-041502/05.

XX P-PSDB; AAU72903.

XX Novel protease polypeptide useful for screening for substances that may
 PT be used to treat, e.g., cancers, immune-related diseases,
 PT cardiovascular disease, migraine, pain, psychotic and inflammatory
 PT disorders

XX Claim 30; Figure 1R-S; 232pp; English.

XX The invention relates to an isolated, enriched, or purified protease
 CC polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to
 CC screen for substances (S) that may modulate its activity. Administering
 CC S (which modulates protease activity in vitro) may be used to treat a
 CC disease or disorder selected from cancers (e.g., of tissues, of blood or
 CC haematopoietic origin, of the breast, colon, lung, prostate, cervical,
 CC brain, ovarian, bladder or kidney), immune-related diseases and
 CC disorders, cardiovascular disease, brain or neuronal-associated diseases
 CC (e.g., central or peripheral nervous system diseases, migraine, pain,
 CC sexual dysfunction, mood disorders, attention disorders, cognition
 CC disorders, hypotension, hypertension, psychotic disorders, neurological
 CC disorders and dyskinesias), metabolic disorders and inflammatory
 CC disorders. (I) may also be useful as a diagnostic tool for a disease or
 CC disorder such as those above. AAS97159-AAS97195 represent human
 CC protease coding sequences and primers of the invention.

XX Sequence 2232 BP; 512 A; 620 C; 705 G; 395 T; 0 other;

alignment_scores:

Quality: 640.50 Length: 115
 Ratio: 5.618 Gaps: 1
 Percent Similarity: 99.130 Percent Identity: 99.130

alignment_block:

US-09-647-780A-4 x AAS97186

Align seg 1/1 to: AAS97186 from: 1 to: 2232

1 GlyHisGluIleThrHisGlyPheAspAspAsn...GlyArgAsnPheAs 16
 1723 GGGCAGGAGATCATCGCACGCGCTTTGACGACAATGGTGGCGGAATTCGA 1772
 16 PysAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisP 33
 1773 CAAGAATGCCAACATGATGGATTGGTGGAGTAACCTTCTCCACCAGCACT 1822
 33 heArgGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTip 49
 1823 TCGGGAGCAGTCAGAGTCATGATCTACCACTACGCACTACTCTCTGG 1872
 50 AspLeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAs 66
 1873 GACCTGGCAGACCAACAGAACGCTGAACGGATTCAACACCCCTTGGGAAAA 1922
 66 nileAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysT 83
 1923 CATGTGCTGACACGAGGGGTGGGCAAGCCTATAAGGCGCTCACTCAAGT 1972
 83 rpMetAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThr 99
 1973 GGATGGCAGAGGGTGGCAAGGACCAAGCAGCTGCCCGGCTGGATCTCACC 2022
 100 HisGluGlnLeuPhePheLeuAsnTyrAlaGlnValTrpCysGly 114
 2023 CATGAGCAGCTCTCTTCATCAACTATGCCAGGTGTGTGGTGGGG 2067
 seq_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAH26248

seq_documentation_block:

ID AAH26248 standard; cDNA; 1124 BP.

XX AC AAH26248;

XX 02-OCT-2001 (first entry)

XX Human secreted protein cDNA clone HSIDD62.

XX Secreted protein; human; HSIDD62; colon cancer; ovary cancer;
 KW tumour; diagnosis; gene therapy; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 2..367
 FT /*tag= a
 FT /partial

XX WO200153343-A1.

XX 26-JUL-2001.

XX 17-JAN-2001; 2001WO-US01436.

XX 18-JAN-2000; 2000US-0176307.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Shi Y;

XX WPI; 2001-483137/52.

XX P-PSDB; AAB82596.

XX Nucleic acid molecules encoding human secreted proteins, used in
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's
 PT diseases and cancers

XX Claim 1(a); Page 330; 339pp; English.

CC The present sequence is that of cDNA clone HSIDD62 (deposited as
CC ATCC PTA1201), which encodes a novel human secreted protein (see
CC AAB82596) that shows homology to atrial natriuretic protein
CC binding protein (ANBP), which is thought to have diuretic
CC (particularly natriuretic) and hypotensive activities. The gene
CC is expressed in adult small intestine tissue as well as in colon
CC tumour tissue and in ovarian cancer tissue. This tissue
CC distribution and homology to human ANBP indicate that
CC polynucleotides, translation products and antibodies corresponding
CC to this gene could be useful in the diagnosis, detection and/or
CC treatment of diseases and/or disorders of the gastrointestinal
CC system, as well as colon tumours and ovarian cancer. Antagonists
CC directed against the gene translation product may be useful in
CC prohibiting or eliminating its biological activities, such as
CC diuretic and hypotensive activities. Vectors, host cells,
CC antibodies, recombinant methods for producing the secreted protein,
CC and screening methods are also provided.
XX
SQ Sequence 1124 BP; 251 A; 362 C; 320 G; 191 T; 0 other;

alignment_scores:
Quality: 603.50 Length: 152
Ratio: 5.294 Gaps: 2
Percent Similarity: 75.000 Percent Identity: 74.342

alignment_block:
US-09-647-780A-4 x AAH26248

Align seg 1/1 to: AAH26248 from: 1 to: 1124

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1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAsp 17
|||||
140 GGGCAGAGATCACCGCGCTTACCAACAATGCCGGAACCTTCGACAA 189

17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
|||||
190 GAATGGCAACATGATGGATTGGTGAGTAACCTCCACCCAGCACTTCC 239

34 rGluGluSerGluCysMetIleThrGlnThrGlyAsnTrpSerTrpAsp 50
|||||
240 GGGACACATCAGAGTGCATGATCTACCACTAGTACGGCACTACTCTCTGGGAC 289

51 LeuAlaAspGluGln Asn..... 56
|||||
290 CTGGCAGACGACACAGACATGAGCGCTGCCACACAGCCAGGCTCGGG 339

56 ..... 56
340 GTACCGGAGCCCGCCAGCTGCGCTGAGGGAGAGGGAAGTCAGGCGCG 389

57 .....ValAsnGlyPheAsnThrLe 63
390 GGCTCCCCCAATCCCTCTCTCTGCGCAGGTGTAACGGATTCAACACCT 439

63 uGlyGluAsnIleAlaAspAsnGlyGlyValArgGlnAlaTyrLysAla 80
|||||
440 TGGGAACAACATGCTGACACGAGGGGTGCGCAANGCCTTAAAGGCCT 489

80 TyrLeuLysTrpMetAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeu 96
|||||
490 ACCTCAAGTGGATGGCAGAGGTGGCAAGGACCAGCAGCTGCCCGCCCTG 539

97 AspLeuThrHisGluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCys 113
|||||
540 GATCTCACCCATGAGCAGCTCTCTCTCATCAACTATGCCAGGTGTGGTG 589

113 sgly 114
|||||
590 CGGG 593
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seq_name: /SID1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH35007

seq_documentation_block:

ID AAH35007 standard; cDNA; 1226 BP.

AC AAH35007;

XX 03-SEP-2001 (first entry)

XX Human colon cancer antigen encoding cDNA SEQ ID NO:2089.

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma; ss.

OS Homo sapiens.

XX WO200122920-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000WO-US26524.

XX 29-SEP-1999; 99US-0157137.

XX 03-NOV-1999; 99US-0163280.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Birse CE, Rosen CA;

XX WPI; 2001-235357/24.

XX P-PSDB; AAG75602.

XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers.

XX Claim 1; Page 3574; 9803pp; English.

XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where
XX the proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene
XX therapy and vaccine production. N and P may be used in the prevention,
XX diagnosis and treatment of diseases associated with inappropriate P
XX expression. For example, N and P may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of P by expressing P.
XX Inactive proteins or to supplement the patients own production of P.
XX Additionally, N may be used to produce the colon cancer-associated Ps,
XX by inserting the nucleic acids into a host cell and culturing the cell
XX to express the proteins. N and P can be used in the prevention, diagnosis
XX and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
XX and AAG77789 represent sequences used in the exemplification of the
XX present invention.

XX N.B. Pages 666 to 682 and page 7053 of the sequence listing were
XX missing at time of publication, meaning no sequences are present for
XX SEQ ID NO:1027 to 1052, 7921 and 7922.

XX Sequence 1226 BP; 270 A; 388 C; 345 G; 213 T; 10 other;

alignment_scores:

Quality: 588.50 Length: 151
Ratio: 5.254 Gaps: 1
Percent Similarity: 74.172 Percent Identity: 74.172

alignment_block:

US-09-647-780A-4 x AAH35007

Align seg 1/1 to: AAH35007 from: 1 to: 1226

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1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAsp 17
|||||
140 GGGCAGAGATCACCGCGCTTACCAACAATGCCGGAACCTTCGACAA 189

17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
```

```
|||||
190 CAATGGCAACATGATGGATGGTGGAGTAACCTTCTCCACCCAGCACTTCC 239
34: rGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpasp 50
|||||
240 GGGAGCAGTCAGAGTGCATGATCTACCACTAGCGGCAACTACTCTCTGGGAC 289
51 LeuAlaAspGluGlnAsn..... 56
|||||
290 TG.GCAGACGACAGCAAGCTGAGCGCTGCCACCACCCAGGCTGGGG 338
56 ..... 56
339 GGTACCGGAGCCYAGCCCTGGCCCTGAGGAGAGGGAAGTCCAGGCGCGG 388
57 ..... ValAsnGlyPheAsnThrLeu 63
|||||
389 GGCTGCCCAATCTCTCTCTGCTGCGCAGTGAACGGATTCAACACCTT 438
64 GlyGluAsnIleAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTy 80
|||||
439 GGGAAACATTTGTGACACAGGAGGGTGGCGCAAGCCTATRAGGCCTA 488
80 rLeuLysTrpMetAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuA 97
|||||
489 CCTCAAGTGGATGGCAGAGGTGGCAAGSACCAGCAGCTGCCCGCCTGG 538
97 sLeuThrHisGluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCys 113
|||||
539 ATCTCACCCATGAGCAGCTCTTCTTCATCACTATGCCAGGTGTGGTGC 588
114 Gly 114
|||
589 GGG 591
```

seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AAA63763

seq_documentation_block:

ID AAA63763 standard; cDNA; 2925 BP.

```
XX AC AAA63763;
XX DT 04-DEC-2000 (first entry)
XX DE cDNA encoding neutral endopeptidase metalloproteinase-like enzyme NL-1.
XX KW Neprilysin; neutral endopeptidase metalloproteinase-like enzyme;
XX KW NEP-like enzyme; protein production; protein secretion;
XX KW neurological disease; Alzheimer's disease; pain; psychiatric disorder;
XX KW fertility; bone disease; abnormal phosphate metabolism; ss.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT CDS 332..2629
XX FT /*tag= a
XX FT /product= "neutral endopeptidase metalloproteinase-like
XX FT enzyme NL-1"
XX PN W0200047750-A2.
XX PD 17-AUG-2000.
XX PF 11-FEB-2000; 2000MO-CA00147.
XX PR 11-FEB-1999; 99CA-2260376.
XX PA (UYMO-) UNIV MONTREAL.
XX PI Desrochers L, Boileau G;
XX PI WPI; 2000-549148/50.
XX DR P-PSDB; AAB08130.
```

```
XX Novel neutral endopeptidase-like metalloproteinase polypeptides and
PT polynucleotides, used to screen for related sequences and enzyme
PT inhibitors, used for the treatment of NL-3 related bone disorders
XX Disclosure; Fig 3; 59pp; English.
XX The present sequence encodes a murine neutral endopeptidase
CC metalloproteinase-like enzyme, designated NL-1. The specification
CC also describes NL-2 and NL-3. The NL enzymes are used to test for
CC specific inhibitors. The N-terminal region of the enzymes can be used
CC to promote production and secretion of foreign proteins and active
CC biopeptides, using chimeric constructs containing the foreign protein
CC downstream from and in phase with the N-terminal region. The NL enzymes
CC are have been localised to the brain, and may be useful in the
CC treatment of neurological diseases such as Alzheimer's disease, pain,
CC and psychiatric disorders. NL enzymes have also been localised to the
CC testis and ovaries, and may be used to control fertility. They have
CC also been localised to bones, and may be used to treat bone disease,
CC and abnormal phosphate metabolisms related to improper peptide
CC processing by the NL-3 enzyme.
XX Sequence 2925 BP; 710 A; 797 C; 836 G; 582 T; 0 other;
```

alignment_scores:

Quality: 581.00 Length: 114
Ratio: 5.142 Gaps: 0
Percent Similarity: 99.123 Percent Identity: 85.088

alignment_block:

US-09-647-780a-4 x AAA63763

Align seg 1/1 to: AAA63763 from: 1 to: 2925

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1 GlyHisGluIleThrHisGlyPheAspAsnGlyValArgAsnPheAsp 17
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2123 GGGCAGCATGATCACACGGCTTTGATGATATGTCGTAACCTTTCACAA 2172
17 sAsnGlyAsnMetMetAspTrpSerAsnPheSerThrGlnHisPheA 34
|||||
2173 GAACGGCAACATGCTGGACTGGTGGAGTAACCTTCGCGCCGCACTTC 2222
34 rGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpasp 50
|||||
2223 AACAGCAGTCGCAATGATCATCTATCAGTACGCAACTCTCTGGAA 2272
51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsn 67
|||||
2273 CTAGCAGACAAACAGAAATGTGAACGGATTTCAGTACCTCGGGGAGAACAT 2322
67 eAlaAspAsnGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
|||||
2323 TCCCGACACAGGAGGTGTCGACAGCATACAGGCTTACCTACGGTGGC 2372
84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
|||||
2373 TGGCTGATGGCGCAAGATCAGCGACTGCCGGGACTGAACCTGACCTAT 2422
101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGly 114
|||||
2423 GCCCAGCTTTTCTTCATCACTAATGATGCCAGGTGTGGTGGG 2464
```

seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAZ28810

seq_documentation_block:

ID . AAZ28810 standard; cDNA; 2765 BP.

```
XX AC AAZ28810;
XX DT 01-FEB-2000 (first entry)
XX DE Rat membrane metalloproteinase NEPII gene.
```

xx Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation;
 KW neuron; hormone; peptide messenger; inhibitor; detection; disorder;
 KW cardiovascular disease; neurodegenerative disease; growth disorder;
 KW hypothalamic-hypophyseal axis; endocrine disorder; ds.
 XX
 OS Rattus rattus.
 XX
 PN FR2777291-Al.
 XX
 PD 15-OCT-1999.
 XX
 PF 08-APR-1998; 98FR-0004389.
 XX
 PR 08-APR-1998; 98FR-0004389.
 XX
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Ouimet T, Gros C, Haret C, Bonhomme MC, Facchinetti P;
 PI Schwartz JC;
 XX
 DR WPI: 1999-593429/51.
 DR P-PSDB; AAY44177.
 XX
 PT New membrane metalloprotease NEP II, involved in proteolysis of
 PT neuronal and hormonal peptides, used to screen for inhibitors.
 PT potentially useful for treating e.g. cardiovascular disease.
 XX
 PS Claim 2; Page 12-16; 29pp; French.
 XX
 CC This sequence represents the gene for the rat membrane metalloprotease
 CC designated neprilysine II (NEPII), which is involved in (in)activation
 CC of neuronal and hormonal peptide messengers. NEPII is used to screen
 CC for specific substrates (used to detect NEPII in cells and tissues) or
 CC inhibitors, which can also be used to detect NEPII or for treatment of
 CC disorders related to peptidergic signalling in which NEPII is involved,
 CC e.g. cardiovascular or neurodegenerative diseases; growth disorders of
 CC endocrine origin; disturbances of the hypothalamic-hypophyseal axis or
 CC endocrine disorders.
 XX
 SQ Sequence 2765 BP; 684 A; 735 C; 787 G; 559 T; 0 other;

alignment_scores:
 Quality: 578.00 Length: 114
 Ratio: 5.115 Gaps: 0
 Percent Similarity: 99.123 Percent Identity: 85.088
 alignment_block:
 US-09-647-780A-4 x AA228810
 Align seg 1/1 to: AA228810 from: 1 to: 2765
 1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAspLy 17
 1925 GGACACGAGATCACACGCGTTTGTATGATAACGTCGGAACCTTTGACAA 1974
 17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
 1975 GAATGGCAACATGCTGGACTGGTGAGCAACTTCTCGGCCCGGCACCTTCC 2024
 34 rgGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50
 2025 GACAGCAGTCACAGTGTATGATTATCATAGTACGCAACTTCTCTTGGGAA 2074
 51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsnII 67
 2075 CTACGACGACACACAGATGTGACGCGATTTCAGCACCTTCGGGGAGAACAT 2124
 67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
 2125 CGCGCAACAACGGCGTGTGCGCGAGGCATACAAGCTTACCTACAGTGGC 2174

84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
 2175 TAGCTGAAGCGCGGACACGAGACTGCCGGGACTGAACCTGACCTAT 2224
 101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGly 114
 2225 GCTCAGCTTTTCTTCATTAACTATGCCAGGTGTGTGTGG 2266
 seq_name: /SIDS1/gcdata/geneseq/geneseq-nbml/NA1988.DAT.AAN81690
 seq_documentation_block:
 ID AAN81690 standard; DNA; 3369 BP.
 XX
 AC AAN81690.
 XX
 DT 23-NOV-1990 (first entry)
 XX
 DE Atrial natriuretic polypeptide binding polypeptide encoding gene.
 XX
 KW Diuretic; atrium cardis; atrial natriuretic peptide binding;
 KW hypotensive action; ss.
 XX
 FH Key Location/Qualifiers
 CDS 23..2272
 FT /*tag= a
 FT /product=atrial natriuretic polypeptide binding peptide
 XX
 PN JP63079598-A.
 XX
 PD 09-APR-1988.
 XX
 PF 22-SEP-1986; 86JP-0222192.
 XX
 PR 22-SEP-1986; 86JP-0222192.
 XX
 PA (SUNR) SUNTORY LTD.
 XX
 DR WPI: 1988-137132/20.
 DR P-PSDB; AAP82940.
 XX
 XX Novel polypeptide, with diuretic action - is obtd. from atrium cardis
 PT of mammals showing specific bond to atrial natriuretic polypeptide
 PT and gene coding it.
 XX
 PS Disclosure; ; p; Japanese.
 XX
 CC The peptide encoded by the gene specifically binds to atrial
 CC natriuretic polypeptide (ANP) and has diuretic (partic. natriuretic)
 CC and hypotensive action.
 CC See also AAN81690-93 and AAP81282-P81309.
 XX
 SQ Sequence 3369 BP; 1110 A; 595 C; 691 G; 973 T; 0 other;

alignment_scores:
 Quality: 471.00 Length: 114
 Ratio: 4.402 Gaps: 0
 Percent Similarity: 93.860 Percent Identity: 66.667
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 US-09-647-780A-4 x AAN81690
 Align seg 1/1 to: AAN81690 from: 1 to: 3369
 1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAspLy 17
 1769 GGACACGAAATCACCCATGGCTTCGATGACAAATGCAGAAATTTTAAACA 1818
 17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
 1819 GGATGGAGACCTTGTGTGACTGTGTGACTCAACAGTCTGCAAAATAATTTTA 1868
 34 rgGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50

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1869 AAGAACAATCCCAATGATGTTGTTACCACTATGGAACACTCTCTCTGGGAC 1918
51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsn11 67
1919 CTAGCAGGTGGACGACATCTCAATGGAATTAATACACTGGGAGAAACAT 1968
67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
1969 TGTGATACGGTGTATGTGCCAGCATACAGACCTCAAAATATG 2018
84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
2019 TTAAAGACAATGTTCAAGAAAATTAATCTCTCGGACTTGACCTAAATCAT 2068
101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGly 114
2069 AACCAACTGTTCTTCTGAACCTCGCCAGGTGTGTGTGGG 2110

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seq_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.AAN80952

seq_documentation_block:

ID AAN80952 standard; DNA; 3181 BP.

XX AAN80952;

DT 15-NOV-1990 (first entry)

XX Enkephalinase gene (human).

XX Enkephalinase; immunosuppressant; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 3..2249

FT /tag= a

FT /product=enkephalinase

XX EP272928-A.

XX 23-DEC-1987; 87EP-0311365;

XX 12-JAN-1987; 87US-0002478.

XX 24-DEC-1986; 86US-0946566.

XX 12-JAN-1987; 87US-0002478.

XX (GETH) GENENTECH INC.

XX Malfroy-Camine B, Scofield PR;

XX WPI; 1988-177004/26.

XX Deoxyribonucleic acid isolates coding for enkephalinase - and prodn
 of enkephalinase, used in therapeutic applications in diagnostic
 immunoassay and as immunosuppressants.

XX Disclosure; ; p; English.

XX The DNA was sequenced from clones isolated from a lambda gt10
 library constructed from poly(A+) human placental RNA. At posn.
 1413 one clone, lambdaH7 was observed to have a G (coding for Ala);
 in clone lambdaH5 this was found to be an A (Thr). Since the former
 is identical to the rat amino acid at posn. 465, the latter
 probably represents an error of the reverse transcriptase synthesis
 of the mRNA. The DNA can be ligated into an expression vector for
 prodn. of the enkephalinase protein in a host. The recombinant
 protein is useful in the treatment of various pathological disor-
 ders associated with endogenous peptides such as tachykinins and
 kinins, eg. acute inflammation, and hyperimmune responses. It's
 also useful in diagnostic immunoassays, and as immunosuppressants
 by virtue of their ability to digest chemotactic molecules.

CC This sequence is also published in EP-272929.
 CC See also AAN80950, AAN80951 and AAN82261.
 XX
 SQ Sequence 3181 BP; 1056 A; 584 C; 653 G; 887 T; 1 other;

alignment_scores:
 Quality: 469.00 Length: 114
 Ratio: 4.383 Gaps: 0
 Percent Similarity: 93.860 Percent Identity: 66.667

alignment_block:

US-09-647-780A-4 x AAN80952

Align seg 1/1 to: AAN80952 from: 1 to: 3181

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1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAsp17
|||||
1743 GGACACGAAATCACCCATGGCTTCGATGACAATGGCAGAACTTTAACAA 1792
17 sasnglyAsnMetMetAspTrpSerAsnPheSerThrGlnHisPheA 34
|||||
1793 AGATGGAGACCTCGTTGACTGTGGTCAACAGTCTGCAAGTAACCTTA 1842
34 rgGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50
|||||
1843 AGAGCAATCCAGTCATGGTGTATCAGTATGGAACCTTTCTCTGGGAC 1892
51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsn11 67
|||||
1893 CTGGCAGGTGGACAGCACCTTAATGGAATTAATACACTGGGAGAAACAT 1942
67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
|||||
1943 TGTGATAATGGAGTCTTGGTCAAGCATACAGAGCCTATCAGAATTATA 1992
84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
|||||
1993 TTAAAGACAATGCGGAGAAATAATTAATCTCTCGGACTTGACCTAAATCAT 2042
101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGly 114
|||||
2043 AACCAACTATTTCTTGAACCTTGACAGGTGTGTGTGGG 2084

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seq_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.AAQ62678

seq_documentation_block:

ID AAQ62678 standard; cDNA; 3181 BP.

XX AAQ62678;

XX 05-JAN-1995 (first entry)

XX Human enkephalinase cDNA.

XX Human; enkephalinase; neutral endopeptidase; kidney; intestine; kinin;
 KW kidney brush border neutral proteinase; pituitary; brain; lymph nodes;
 KW neutrophils; enkephalins; tachykinins; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 3..2249

FT /tag= a

FT mat_peptide 21..2246

FT /tag= b

FT allele 1413

FT /tag= c

FT /note= "Nucleotide is A in a different clone

FT changing the codon to Thr"

XX EP596355-A.

PD 11-MAY-1994.
XX
XX 23-DEC-1987; 87EP-0117230.
XX
XX 24-DEC-1986; 86US-0946566.
PR 12-JAN-1987; 87US-0002478.
XX
XX (GETH) GENENTECH INC.
XX
XX Malfroy-Camine B, Schofield PR;
PI
XX WPI; 1994-152785/19.
DR P-PSDB; AAR52706.
XX
XX Method for assay of enkephalinase using dansylated peptide(s) -
PT for identification of recombinant enkephalinase
PT
XX Disclosure; Fig 1; 61pp; English.
XX
XX This sequence encodes human enkephalinase. Enkephalinase is a
CC neutral endopeptidase or kidney brush border neutral proteinase. It
CC has been isolated from the kidney, intestine, pituitary, brain and
CC lymph nodes, and has been detected in many peripheral organs and in
CC human neutrophils. The distribution of enkephalinase in the brain
CC closely parallels the distribution of the enkephalins. Mammalian
CC enkephalinase may be used in the treatment of various pathological
CC disorders associated with various endogenous peptides, eg.
CC tachykinins and kinins.
XX
XX Sequence 3181 BP; 1055 A; 582 C; 657 G; 887 T; 0 other;
SQ

alignment_scores:
Quality: 469.00 Length: 114
Ratio: 4.383 Gaps: 0
Percent Similarity: 93.860 Percent Identity: 66.667

alignment_block:
US-09-647-780A-4 x AA062678

Align seg 1/1 to: AA062678 from: 1 to: 3181

1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAsp 17
|||||
1743 GGACACGAATCACCCTGGCTTCGATGACATGGCAGAACTTTAACAA 1792
|||
17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
|||
1793 AGATGGAGACCTCGTTGACTGGTGGACTCAACAGTCTGCAAGTAACTTTA 1842
|||
34 rgGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50
|||||
1843 AGGACCAATCCAGTCAGTGGTGTATCATGATGGAACCTTTCTCGGGAC 1892
|||
51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsn 67
|||||
1893 CTGGCAGGTGGACACACCTTAATGAATTAATACACTGGGAGAAACAT 1942
|||
67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrp 84
|||||
1943 TGCTCATATGGAGCTCTGGTCAAGCATACAGAGCCATCAGAAATTATA 1992
|||
84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
|||
1993 TTAAGAAAGAAATGGGAGAGAAAAATTAATCTCTGGACTTGACCTAAATCAC 2042
|||
101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGly 114
|||||
2043 AAACAACATAATTTTCTTGAACCTTTCACAGAGTGTGTGGA 2084
|||


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264  CGCCGACAAACGGGGGGCGCTCAAGCGGGCGCTTACGGCGCTACCAAGAACTGGG 313
      84  etAlalacluglyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
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314  TCAAGAGAAATGGGCTGAGCACACACTGCCACCCCTGGGTCTCACCAC 363
      101  GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGlyCysLys 116
      ||| ||||| ||||| ||||| ||||| ||||| |||||:::
364  AACCAAGCTCTTCTCTGTAGTTTTGCACAGGTCTGGTGTTCCGGTCCGC 411
      seq_name: /cqn2_6/ptodata/1/lna/6A_COMB.seq:US-08-646-273-22

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seq_documentation_block:
; Sequence 22, Application US/08646273
; Patent No. 6066502
;
; GENERAL INFORMATION:
; APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,
; APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Heinz
; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
; NUMBER OF SEQUENCES: 36
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinkauf
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.0
; SOFTWARE: Wordperfect version 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646.273
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/03706
; FILING DATE: 11-NOV-1994
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2129 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA for mRNA
; US-08-646-273-22

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alignment_scores:      Quality: 374.50      Length: 116
                       Ratio: 3.901       Gaps: 1
Percent Similarity: 82.759  Percent Identity: 54.310

alignment_block:
US-09-647-780A-4 x US-08-646-273-22

Align seg 1/1 to: US-08-646-273-22 from: 1 to: 2129

1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAsp 17
|||||.....
1632 GCCACGAGCTCAGTCATCTTTGATGATCAAGGCCGAGAGTACGACAA 1681

17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
|||||.....
1682 GGATGGGAACCTCCGGCCCTGGTGGGAAGAACTGTCGCTGGAGCGCGTTCA 1731

34 rGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50
|||||.....
1732 AGCAGGACACCGCGTGCATGGTGGACGACGTACGGCACTATACG..... 1775

51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsn 67
|||||.....

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```

1776 ...GTGAACGGGGAGCGGTGAACGGCCGGCACACCCCTCGGGCGAAACAT 182Z
67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
1823 CGCGCAACACGGGGCGCTCAAGCGCGCCTATCGGCGCTACCAAGAATGG 187Z
84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
1873 TCAAGAGAAGTGGGCGCTGAGGACACACTGCCACCCTGGGTCTCACCAAC 192Z
101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTyrCysGlyCysLys 116
1923 AACAGACTCTTCTCCTGAGTGTTCACAGGCTGGTGTTCGTCGCGC 1970
seq_name: /cgn2_5/ptodata/1/ina/6A_COMB.seq:US-08-646-273-29
seq_documentation_block:
; Sequence 29, Application US/08646273
; Patent No. 606502
; GENERAL INFORMATION:
; APPLICANT: Kroeger, Burkhard, Seuberger, Harald, Meyer, T.
; APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski,
; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinkauf
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage.
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.0
; SOFTWARE: Wordperfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,273
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/03706
; FILING DATE: 11-NOV-1994
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2314 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA for mRNA
;

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alignment_scores:      Quality: 374.50      Length: 116
                        Ratio: 3.901       Gaps: 1
                        Percent Similarity: 82.759    Identity: 54.310

alignment_block:
US-09-647-780A-4 x US-08-646-273-29   ..

Align seg 1/1 to: US-08-646-273-29 from: 1 to: 2314

1 GLVHISGLIuIeThrHisGlyPheAspAsnGLyArgAsnPheAsPLY 17
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1806 GGCCAGGACTGCATCATCTTTTGATGATCAAGCGCGAGTACGACAA 1855

17 sASnGlyAsnMetMetAsPTripSerAsnPheSerThrGlnHisPhea 34
::::|||:::|||||:::|||||:::|||||:::|||||:::|||||
1856 GGATGGGAACCTCCGGCCCCCTGTGTGGAAGAACTCGTCGCTGGAGCGCTTCA 1905

34 rGLuclnSerGlucysMetIleTy rGlnTy rGlyAsnTy rSerTrpasp 50
::::|||:::|||||:::|||||:::|||||:::|||||:::|||||
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1906 AGCAGCAGACCGCGTCGTCATGGTGGAGCAGCTACGGCAACTATATAGC..... 1949
51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsnI1 67
1950GTGAACGGGAGCGCGGTGAACCGCGGCACACCCCTCGGCGAAACAT 1996
67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
1997 CGCCGACAAACGGGCGCTCAAGGCGGCTATCGGCGCTACCAAGAACTGGG 2046
84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
2047 TCAAGAAGATGGGCTGAGCAGACACTGCCACCCCTGGGTCTCCACCAAC 2096
101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGlyCysLys 116
2097 AACCAAGCTCTTCTCTGAGTTTCCACAGGCTCTGGTGTTCGCTCGGC 2144
seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-289-112-1

seq_documentation_block:
; Sequence 1, Application US/08289112
; Patent No. 568640

GENERAL INFORMATION:
; APPLICANT: Yanagisawa, Masashi
; TITLE OF INVENTION: Endothelin Converting Enzyme-1: A
; TITLE OF INVENTION: Membrane-Bound Metalloprotease That Catalyzes The
; TITLE OF INVENTION: Proteolytic Activation of Big Endothelin-1

NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX

COUNTRY: USA
; ZIP: 77210-4433
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; APPLICATION NUMBER: US/08/289,112
; FILING DATE: 10-APR-1994
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:414/PAR
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2889 base pairs
; TYPE: nucleic acid
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:

NAME/KEY: CDS
; LOCATION: 118..2391
US-08-289-112-1

alignment_scores:
Quality: 370.50 Length: 116
Ratio: 3.859
Percent Similarity: 82.759 Percent Identity: 53.448

alignment_block:
US-09-647-780A-4 x US-08-289-112-1

Align seg 1/1 to: US-08-289-112-1 from: 1 to: 2889
1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAspLy 17
1897 GCCCAGCAGCTCAGCTCATCTTTTGTATGATCAAGCGCGAGAGTACGACAA 1946
17 sAsnGlyAsnMetMetAspTyrTrpSerAsnPheSerThrGlnHisPheA 34
1947 GGATGGGAACCTCCGGCCCTGGTGGGAAGAACTCGTCGCGGAGCGCGTTCA 1996
34 rgGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50
1997 AGCAGCAGACCGCGTGCATGGTGGAGCAGTACGGCAACTATAGC..... 2040
51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsnI1 67
2041GTGAACGGGAGCGCGGTGAACCGCGGCACACCCCTCGGCGAAACAT 2087
67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
2088 CGCCGACAAACGGGCGCTCAAGGCGGCTATCGGCGCTACCAAGAACTGGG 2137
84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
2138 TCAAGAAGATGGGCGTGAACGAGACACTGCCACCCCTGGGTCTCCACCAAC 2187
101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGlyCysLys 116
2188 AACCAAGCTCTTCTCTGAGTTTCCACAGGCTCTGGTGTTCGCTCGGC 2235
seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-646-273-24

seq_documentation_block:
; Sequence 24, Application US/08646273
; Patent No. 6066502

GENERAL INFORMATION:
; APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,
; APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Hein
; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE)
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinkauff
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.0
; SOFTWARE: Wordperfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,273
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/03706
; FILING DATE: 11-NOV-1994
INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2533 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA for mRNA
US-08-646-273-24

alignment_scores:
Quality: 367.50 Length: 116
Ratio: 3.750
Gaps: 1


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alignment_scores:
  Quality: 367.50      Length: 116
  Ratio: 3.750         Gaps: 1
  Percent Similarity: 84.483  Percent Identity: 53.448

alignment_block:
  US-09-647-780A-4 x US-08-646-273-35

  Align seg 1/1 to: US-08-646-273-35 from: 1 to: 2720

      1 GlyHisGluIleThrHisGlyPheAspAspAsnGlyArgAsnPheAsp 17
      1802 GCCCATGAGCTGACTCATGCTTTTCATGATCAAGGACGGGAGTATGACAA 1851

      17 sAsnGlyAsnMetMetAspTrrpSerAsnPheSerThrGlnHisPheA 34
      1852 GGACGGGAACCTCCGGCCATGGTGAAGAAGCTATCCTCGTGAGGCGCTTCA 1901

      34 rGluGlnSerGluCysMetIleThrGlnTyrGlyAsnTyrSerTrpAsp 50
      1902 AGCGTCAGACCGAGTGCATGGTAGACAGTAGTACAGAACTACAGC..... 1945

      51 LeuAlaaspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsn 67
      1946 ...GTGAACGGGGAGCCGGGTGAACGGGGCGGCACACCTGGGGAGAACAT 1992

      67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
      1993 CGCCGACAAACGGGGGTCTCAAGCGCGCCTATCGGCTTACCAGAACTGGG 2042

      84 etAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
      2043 TGAAGAAGAACCGGGCTGAGCAGCTCGCTCCCAACCTGGGCGCTCAACCA 2092

      101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGlyCysLys 116
      2093 AACCAGCTCTTCTTCTCGGGCTTTCACACAGGTCCTGGTGTCCGTCGCGC 2140

seq_name: /cgn2 6/ptodata/1/ina/5A_COMB.seq:US-08-574-763-1

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seq documentation block:
; Sequence 1, Application US/08574763.
; Patent No. 5736376
; GENERAL INFORMATION:
; APPLICANT: Yanagisawa, Masashi
; TITLE OF INVENTION: RECOMBINANT ENDOTHELIN CONVERTING
; TITLE OF INVENTION: ENZYME-2 AND ITS USE IN ECE INHIBITOR SCREENING
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,763
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Corder, Timothy S.
; REGISTRATION NUMBER: 38,414
; REFERENCE/DOCKET NUMBER: UTXD:472
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 1:

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SEQUENCE CHARACTERISTICS:
  LENGTH: 3291 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 116..2476
  US-08-574-763-1

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alignment_scores:
  Quality: 339.50      Length: 116
  Ratio: 3.574        Gaps: 1
  Percent Similarity: 81.897  Percent Identity: 50.000

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alignment_block:
  US-09-647-780A-4 x US-08-574-763-1

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Align seg 1/1 to: US-08-574-763-1 from: 1 to: 3291

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1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAspLy 17
|||||
1982 GCCACGAGTTGACACATGCTTTCATGACCAAGGCGCGAGTATGACAA 2031

17 sAsnGlyAsnMetMetAspTTrpTTrpSerAsnPheSerThrGlnHisPheA 34
|||||
2032 GGAAGGAAATCGCGCGCTGTGTCAGCAATGAGTCGTGGCAGCCTTCC 2081

34 rGluGlnSerGluCysMetIleTyrlGlnTyrlGlyAsnTyrSerTrpAsp 50
|||||
2082 GGAACACACGCGCTGATAGAGGAGCAGTACAGCCAGTACCAG ..... 2125

51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsnI 67
|||||
2126 ...GTCAACGGGGAGAGAACTCAACGGCGCCAGACACTGGGGGAGAACAT 2172

67 eAlaAspAsnGlyGlyValArgGlnAlaTyrlGlyAsnTyrLeuLysTrpM 84
|||||
2173 TGCCGCAATGGGGGCTTAGGCTGCTTACACCTTACAAAGCATGGC 2222

84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
|||||
2223 TAAGAAAGCATGGGAGGAGCAGCAGCTGCCAGCTGTGGACTCACCAAC 2272

101 GluGlnLeuPheIleAsnTyrAlaGlnValTrpCysGlyCysLys 116
|||||
2273 CACCAGCTCTTCTTTGTGGGATTTGCCAGGTGTGGTGTCTCGTCCGC 2320

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seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-646-273-18

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seq_documentation_block:
  Sequence 18, Application US/08646273
  Patent No. 6065502
  GENERAL INFORMATION:
    APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,
    APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Heinz.
  TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
  NUMBER OF SEQUENCES: 36
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Keil & Weinlauf
    STREET: 1101 Connecticut Avenue
    CITY: Washington
    STATE: D.C.
    COUNTRY: USA
    ZIP: 20036
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
    COMPUTER: IBM AT-compatible, 80486 processor
    OPERATING SYSTEM: MS-DOS version 6.0
    SOFTWARE: WordPerfect version 5.1
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/646,273

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FILING DATE: 16-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/EP94/03706
  FILING DATE: 11-NOV-1994
  INFORMATION FOR SEQ ID NO: 18:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1703 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA for mRNA
  US-08-646-273-18

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alignment_scores:
  Quality: 336.50      Length: 106
  Ratio: 3.868        Gaps: 1
  Percent Similarity: 82.075  Percent Identity: 54.717

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alignment_block:
  US-09-647-780A-4 x US-08-646-273-18

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Align seg 1/1 to: US-08-646-273-18 from: 1 to: 1703

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1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAspLy 17
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1394 GCCACGAGCTGACTCATCTTTTGTATGATCAAGCGCGAGTACGACAA 1443

17 sAsnGlyAsnMetMetAspTTrpTTrpSerAsnPheSerThrGlnHisPheA 34
|||||
1444 GATGGGAACCTCCGGCCCTGGTGGGAAGAACTGTCGCGGAGCGCTTCA 1493

34 rGluGlnSerGluCysMetIleTyrlGlnTyrlGlyAsnTyrSerTrpAsp 50
|||||
1494 AGCAGCAGACCGCGTGCATGTGTGGAGCAGTACGGCAACTATAGC ..... 1537

51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsnI 67
|||||
1538 ...GTGAACGGGGAGCGCGGTGAACGGCGGCACACCTCGCGGAAAACAT 1584

67 eAlaAspAsnGlyGlyValArgGlnAlaTyrlGlyAsnTyrLeuLysTrpM 84
|||||
1585 CCGCCACACACGGGGGCTCAGCGCGCTATCGGCGCTACCGAAGCTGGG 1634

84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
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1635 TCAGAGAGATGGGCTGAGCAGACACTGCCACCTGGGTCTCACCACAC 1684

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101 GluGlnLeuPheIle 106

1685 AACCACTCTTCTCTG 1702

seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-305-640-1

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seq_documentation_block:
  Sequence 1, Application US/09305640B
  Patent No. 6255468
  GENERAL INFORMATION:
    APPLICANT: SmithKline Beecham plc
    TITLE OF INVENTION: No. 6255468el Compounds
    FILE REFERENCE: GP30124
    CURRENT APPLICATION NUMBER: US/09/305,640B
    CURRENT FILING DATE: 1999-05-05
    NUMBER OF SEQ ID NOS: 4
    SOFTWARE: FastSeq for Windows Version 3.0
    SEQ ID NO 1
    LENGTH: 2560
    TYPE: DNA
    ORGANISM: Homo sapiens
  US-09-305-640-1

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alignment_scores:
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  Ratio: 3.703        Gaps: 1
  Percent Similarity: 76.106 Percent Identity: 49.558
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2056 GGACATGAGCTGACCCACGGCTACGACGCTGGGGCCAGTATGACCG 2105
17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2106 CTCAGGGAACCTGCTGCACTGGTGACGAGGCGCTTACAGCCGCTCC 2155
34 rGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50
|||||:|||||:|||||:|||||:|||||:|||||:
2156 TCGGAAGCGTGAGTGCACTGCTCTATGACAACTTCACT..... 2199
51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsn 67
|||:|||||:|||||:|||||:|||||:|||||:|||||:
2200 ...GCTACACACCGCGTGAACGGAACACACGCTGGGGAGAACAT 2246
67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
|||||:|||||:|||||:|||||:|||||:|||||:
2247 CGCAGATATGGCGCCCTCAAGCTGGCTTACCACGCTATCAGAAAGTGG 2296
84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
|||:|||||:|||||:|||||:|||||:|||||:
2297 TCGCGGACGACGCGCCAGACGACCCACTTCCCGGCTCAAGTACACAT 2346
101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCys 113
|||||:|||||:|||||:|||||:|||||:
2347 GACCAGCTCTTCTTCACTGCTTCCCTTCCCGGAGACTGGTGC 2385
seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-305-640-3
seq_documentation_block:
; Sequence 3, Application US/09305640B
; Patent No. 6255468
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham plc
; TITLE OF INVENTION: No. 6255468el Compounds
; FILE REFERENCE: GP30124
; CURRENT APPLICATION NUMBER: US/09/305,640B
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version. 3.0
; SEQ ID NO 3
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (404)(437)(460)(490)(520)(555)(561)(595)
US-09-305-640-3
alignment_scores:
  Quality: 112.50      Length: 83
  Ratio: 1.907        Gaps: 5
  Percent Similarity: 71.084 Percent Identity: 42.169
alignment_block:
US-09-647-780A-4 x US-09-305-640-3
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1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAsp 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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305 GGACATGAGCTGACCCACGGCTACGACGAGCTGGGGCCAGTATGACC 354
17 ysAsnGlyAsnMetMetAspTrpTrp...SerAsnPheSerThrGlnHis 32
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
355 GCTCAGGGAACCTGCTGCACTGGTGGGACGAGGCTTCCTTTACAGCCGN 404
32 spHeArgGluGlnSerGluCysMetIle...TyrGlnTyrGlyAsnTyrSe 48
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
405 TTCTCTGCGAAGGCTGAGTGCATGCTCCCTNTTTTATGGACAACCTTC 454
48 rTrpAspLeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyG 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
455 A.....ATGTTNTTACAACGAGCGGTGAACGGGAA.ACACANGTTTGGG 497
65 luAsnIleAlaAspAsnGlyGlyValArgGlnAlaTyrLysAla 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
498 AGAACATCGCAGTATGGGGCGGNCCTTAAGTTGGCTTACCACGCT 541
seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-258-188-1
seq_documentation_block:
; Sequence 1, Application US/08258188
; Patent No. 5475098
; GENERAL INFORMATION:
; APPLICANT: HALL, Robert H.
; APPLICANT: XU, Jian Guo
; TITLE OF INVENTION: A NEW AND DISTINCTIVE DNA SEQUENCE OF E.
; TITLE OF INVENTION: coli 0157:H7 AND ITS USE FOR THE RAPID, SENSITIVE AND
; TITLE OF INVENTION: SPECIFIC DETECTION OF 0157:H7 AND OTHER ENTEROHEMORRHAGIC
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,188
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 15280206, DHHSE135940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2278 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (plasmid)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..2275
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..2278
; OTHER INFORMATION: /product= "Peptide encoded by the
; OTHER INFORMATION: hlyA gene"
; OTHER INFORMATION: /standard_name= "Nucleic acid sequence of hlyA
; OTHER INFORMATION: gene"
US-08-258-188-1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2278 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (plasmid)
FEATURE:
NAME/KEY: CDS
LOCATION: 2..2275
NAME/KEY: misc_feature
LOCATION: 1..2278
OTHER INFORMATION: /product= "Peptide encoded by the hlyA gene".
OTHER INFORMATION: hlyA gene".
OTHER INFORMATION: /standard_name= "Nucleic acid sequence of hlyA gene"
US-08-526-813-1

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Quality: 73.00 Length: 91,
Ratio: 1.521 Gaps: 4
Percent Similarity: 52.747 Percent Identity: 24.176

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US-09-647-780A-4 x US-08-526-813-1
Align seg 1/1 to: US-08-526-813-1 from: 1 to: 2278

10 AspAsnGlyValArgAsnPheAspLysAsnGly..... 19
:::|||||:::|||||:::|||||
542 GACCATGGCAAAATATTATTTTTCAGATGGATATGACCGAAGACATGCTGC 591
20 .....AsnMetMetAspTrpSerAsnPheSerThrGlnHisP 33
592 GTTTTTAGAAGACTCTCTGCTTTTGCTGTGATTTTCTCGTCAGCATG 641
33 hearGluGlnSerGluCysMetIleTyrglnTyrclyAsnTrpSerTrp 49
|||||:::|||||:::|||||
642 CAGTAGAAGAGCAGTCGCAATAACCACGACAACAT.....TGG 679
50 AspleuAlaaspgluGlnAsnValAsnGlyPheAsnThrLeuGlyclu... 65
|||:::|||||
680 GAT.....GAGAAGATCGGTGAAC 699
66 ...AsnIleAlaaspAsnGlyGlyValArgGlnAlatyrLysAlatyrL 81
|||||:::|||||
700 TGCAGGCATTAACCCGTAATGCTGATCGCAGTCAGACTGCTGAAGGCATATA 749
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seq_documentation_block:
; Sequence 1, Application PC/TUS9508554
GENERAL INFORMATION:
APPLICANT: XU, Jian Guo
TITLE OF INVENTION: A NEW AND DISTINCTIVE DNA SEQUENCE OF E. COLI O157:H7 AND ITS USE FOR THE RAPID, SENSITIVE AND SPECIFIC DETECTION OF O157:H7 AND OTHER ENTEROHEMORRHAGIC ESCHERICHIA COLI STRAINS
TITLE OF INVENTION: E. coli
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
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seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-526-813-1

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seq_documentation_block:
  Sequence 1, Application US/08526013
  Patent No. 5756293
  GENERAL INFORMATION:
    APPLICANT: Hall, Robert H.
    APPLICANT: Xu, Jian Guo
    TITLE OF INVENTION: A New and Distinctive DNA Sequence of E.
    Patent No. 5756293
    TITLE OF INVENTION: coli O157:H7 and its Use for the Rapid, Sensitive and
    TITLE OF INVENTION: Specific Detection of O157:H7 and Other Enterohemorrhagic
    TITLE OF INVENTION: E. coli
    NUMBER OF SEQUENCES: 29
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Townsend and Townsend and Crew LLP
      STREET: Two Embarcadero Center, Eighth Floor
      CITY: San Francisco
      STATE: California
      COUNTRY: USA
      ZIP: 94111-3834
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent In Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/526,813
        FILING DATE: 11-SEP-1995
        CLASSIFICATION: 435
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 08/258,188
        FILING DATE: 14-JUN-1994
      ATTORNEY/AGENT INFORMATION:
        NAME: Garrett-Wackowski, Eugenia
        REGISTRATION NUMBER: 37,330
        REFERENCE/DOCKET NUMBER: 15280-206-1

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seq_documentation_block:
; Sequence 54, Application US/08484570A
; Patent No. 5804379
; GENERAL INFORMATION:
; APPLICANT: Lee, Soohye
; APPLICANT: Redman, Colvin L.
; TITLE OF INVENTION: Diagnostic Method and Kit for
; TITLE OF INVENTION: Determining Kell Blood Group
; TITLE OF INVENTION: Genotype
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ronald J. Baron, Esq.
; ADDRESSEE: Hoffmann & Baron
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: USA
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,570A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/337,268
; FILING DATE: 11-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Baron, Ronald J.
; REGISTRATION NUMBER: 29,281
; REFERENCE/DOCKET NUMBER: 454-3 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; US-08-484-570A-54

alignment_scores:
Quality: 72.00 Length: 37
Ratio: 2.880 Gaps: 0
Percent Similarity: 67.568 Percent Identity: 43.243

alignment_block:
US-09-647-780A-4 x US-08-484-570A-54
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:::||||| ||| :::: ||||
23 CAGCAATACAGCAGCGCTGTTCAGCACCATGGGAGACTGTCCTGCC 72
|:::|||||::: |:::|||||::: |||||
94 oGlyLeuAspLeuThrHisGluGlnLeuPhePheIleAsnTyrAlaGlnV 111
|:::|||||::: |:::|||||::: |||||
73 CAGCCTGACCTCAGCCCCCAGCAGACTCTTCTTCGAGAGCTATGCCAGG 122
|||
111 altrpCysGly 114
||
123 TAGCAGCGGC 133
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 3, 2002, 11:05:27 ; Search time 30.1 Seconds
(without alignments)
428.058 Million cell updates/sec

Title: US-09-647-780A-4
Perfect score: 665
Sequence: 1 GHEITHGDDNGRNFDPKNGN.....DLTHQLFFINAYQVWCCK 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	651	97.9	702	22	AA83844 Amino acid sequenc
3	651	97.9	753	22	AA83842 Amino acid sequenc
4	651	97.9	753	22	AA860562 Human neprilysin-1
5	651	97.9	762	22	AA860563 Human neprilysin-1
6	651	97.9	770	21	AA808131 A human neutral en
7	651	97.9	779	22	AA83841 Amino acid sequenc
8	651	97.9	779	22	AA860561 Human neprilysin-1
9	581	87.4	765	21	AA808130 A murine neutral e
10	578	86.9	774	20	AA844177 Rat membrane metal
11	471	70.8	750	9	AA82940 Atrial natriuretic

12	469	70.5	743	22	AAE07916 Human neutral endo
13	469	70.5	743	22	AAE07952 Human neutral endo
14	469	70.5	743	22	AA85104 Human enkephalinas
15	469	70.5	743	22	AA85115 Human enkephalinas
16	469	70.5	748	9	AA80969 Enkephalinase (hum
17	469	70.5	748	15	AA852706 Human enkephalinas
18	469	70.5	750	10	AA852706 Human enkephalinas
19	465	69.9	255	13	AA822040 Human common acute
20	465	69.9	750	9	AA822040 Short-form rat enk
21	465	69.9	750	9	AA82867 Enkephalinase (rat
22	397.5	59.8	661	22	AA822707 Enkephalinase.
23	374.5	56.3	189	16	AA861898 Drosophila melanog
24	374.5	56.3	708	16	AA876234 Bovine endothelin
25	374.5	56.3	754	16	AA876236 Bovine foetal hear
26	370.5	55.7	758	19	AA876226 Bovine endothelin
27	367.5	55.3	703	16	AA876237 Bovine endothelin
28	367.5	55.3	753	16	AA875691 Human placental en
29	367.5	55.3	753	16	AA876227 Endothelin convert
30	367.5	55.3	758	17	AA876227 Human endothelin c
31	367.5	55.3	758	17	AA876227 Human endothelin c
32	353	53.1	749	19	AA803736 Amino acid sequenc
33	353	53.1	749	21	AA853457 Human PHEX. Homo
34	353	53.1	749	21	AA853457 Amino acid sequenc
35	343.5	51.7	883	22	AA867845 Polypeptide homolo
36	339.5	51.1	736	20	AA841774 Human PRO403 prote
37	339.5	51.1	736	21	AA844330 Human PRO403 prote
38	339.5	51.1	736	22	AA829233 Human PRO polypept
39	339.5	51.1	787	19	AA837750 Amino acid sequenc
40	338.5	50.9	763	22	AA864640 Drosophila melanog
41	336.5	50.6	567	16	AA876235 Bovine foetal hear
42	336	50.5	121	22	AA82596 Human secreted pro
43	323	48.6	726	22	AA861546 Drosophila melanog
44	320	48.1	112	22	AA82599 Human secreted pro
45	320	48.1	129	22	AA875602 Human colon cancer

ALIGNMENTS

RESULT 1

AA83840
ID AA83840 standard; Protein; 691 AA.

XX AA83840;

XX AA83840;

DT 23-JUL-2001 (first entry)

XX Amino acid sequence of a human metalloprotease enzyme IGS5.

XX Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity; -
anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
KW hypotension; hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; stroke; ulcer; allergy;
KW benign prostatic hypertrophy; migraine; psychotic disorder;
KW neurological disorder; autism; multiple sclerosis; kidney disease;
KW neurodegenerative disease; sleep disorder; Alzheimer's disease;
KW cardiovascular disease; arteriosclerosis; cerebrovasospasm;
KW subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
KW peripheral vascular disease; Raynaud's disease; motility disorder;
KW gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
KW inflammation; chemotherapy induced injury; tumour invasion;
KW immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
KW severe mental retardation; dyskinesia; Huntington's disease;
Gilles de la Tourette's syndrome.

OS Homo sapiens.

PN WO200136610-A1.

XX 25-MAY-2001.

PF 17-NOV-2000; 2000WO-EPI1532.

XX

QY 1 GHEITHGFDNDRNFKNMMDWMSNFSTQHFQSCMIYQYGNYSWDLADEQNVNGF 60
Db 535 gheithgfdngnfrdnknmmdwmsnfstqhfqscmlyqygnyswldadeqnvngf 594
QY 61 NTLGENTADNGGVQYKAYKAYLKWMAEGGKQDLPLDLTHTHEQLFFINVAQVWCG 114
Db 595 ntlgeniadnggvrgaykaylkwmaeggkdqqlpdlthcheqlffinyavqvcg 648

RESULT 3

AAB83842
ID AAB83842 standard; Protein: 753 AA.

XX AAB83842;

XX 23-JUL-2001 (first entry)

DE Amino acid sequence of a human metalloprotease enzyme. IGS5.

XX Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity;
KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
KW hypertension; hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; stroke; ulcer; allergy;
KW benign prostatic hypertrophy; migraine; psychotic disorder;
KW neurological disorder; autism; multiple sclerosis; Alzheimer's disease;
KW neurodegenerative disease; sleep disorder; epilepsy; kidney disease;
KW cardiovascular disease; arteriosclerosis; cerebrovasospasm;
KW subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
KW peripheral vascular disease; Raynaud's disease; motility disorder;
KW gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
KW inflammation; chemotherapy induced injury; tumour invasion;
KW immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
KW severe mental retardation; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome.

XX Homo sapiens.

XX WO200136610-A1.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000WO-EP11532.

XX 19-NOV-1999; 99EP-0203862.

XX 19-NOV-1999; 99NL-1013616.

XX 31-MAY-2000; 2000EP-0201937.

XX 31-MAY-2000; 2000NL-1015356.

XX (SOLV) SOLVAY PHARM BV.

XX Deleersnijder W, Wiegers R, Weske M;

XX WPI; 2001-343815/36.

XX N-PSDB; AAF89739.

XX New IGS5 polypeptides useful for treating infections, pain, cancer,
PT diabetes, obesity, anorexia, bulimia, asthma, schizophrenia,
PT hypertension, urinary retention and Parkinson's disease

XX Claim 3; Page 9-10; 115pp; English.

XX The present sequence represents a human metalloprotease enzyme designated
CC IGS5. IGS5 polynucleotides and polypeptides are useful for treating
CC infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma,
CC Parkinson's disease, acute heart failure, hypotension, hypertension,
CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC stroke, ulcers, allergies, benign prostatic hypertrophy, migraine,
CC psychotic and neurological disorders, autism, multiple sclerosis,
CC Alzheimer's disease, and other neurodegenerative diseases, sleep
CC disorder, epilepsy, cardiovascular diseases, arteriosclerosis,
CC cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral
CC infarction, peripheral vascular disease, Raynaud's disease, kidney
CC diseases, gastrointestinal disorders, motility disorders and conditions

CC of delayed gastric emptying, post-operative or diabetic gastroparesis,
CC diarrhoea, inflammations, chemotherapy induced injury, tumour invasion,
CC immune disorders, arthritis, endotoxin shock, sepsis, complications of
CC diabetes mellitus, and severe mental retardation and dyskinesias, such
CC as Huntington's disease or Gilles de la Tourette's syndrome.

XX Sequence 753 AA;

Query Match 97.9%; Score 651; DB 22; Length 753;

Best Local Similarity 100.0%; Pred. No. 6.7e-64;

Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHEITHGFDNDRNFKNMMDWMSNFSTQHFQSCMIYQYGNYSWDLADEQNVNGF 60

Db 586 gheithgfdngnfrdnknmmdwmsnfstqhfqscmlyqygnyswldadeqnvngf 645

QY 61 NTLGENTADNGGVQYKAYKAYLKWMAEGGKQDLPLDLTHTHEQLFFINVAQVWCG 114

Db 646 ntlgeniadnggvrgaykaylkwmaeggkdqqlpdlthcheqlffinyavqvcg 699

RESULT 4

AAB60562

ID AAB60562 standard; Protein: 753 AA.

XX AAB60562;

XX 27-APR-2001 (first entry)

XX Human neprilysin-like membrane metalloproteinase SNEPB.

XX Human; SNEPB; neprilysin-like membrane metalloproteinase;
KW splice variant; alternative splicing; zinc endopeptidase family;
KW neuropeptide; peptide hormone; processing; metabolism; vaccine;
KW drug screening; renal insufficiency; hepatic disease; ischaemia; pain;
KW hypertension; cancer; inflammation; cardiovascular disease;
KW neuronal disease; pancreatic disease; prostatic disease;
KW respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic;
KW cerebroprotective; hypotensive; cytostatic; antinflammatory;
KW cardiovascular; hepatotropic.

XX Homo sapiens.

XX EPI069188-A1.

XX 17-JAN-2001.

XX 15-JUL-1999; 99EP-0401767.

XX 15-JUL-1999; 99EP-0401767.

XX (SNF1) SANOFI-SYNTHELABO.

XX Jagerschmidt A, Agnel M, Culouscou J;

XX WPI; 2001-212582/22.

XX N-PSDB; AAF59660.

XX New membrane-associated metalloproteinase SNEPB, SNEPB and SNEPC
PT polypeptides and polynucleotides, useful for treating e.g. acute and
PT chronic renal insufficiency, pain, stroke, cancer, inflammation, renal
PT and hepatic ischemia

XX Claim 11; Page 33-35; 72pp; English.

XX The invention relates to the human SNEPB, SNEPB and SNEPC proteins, and
CC the cDNAs encoding them. SNEPB, SNEPB and SNEPC are neprilysin-like
CC membrane metalloproteinases and are the products of alternative splicing.
CC The substrate(s) for the SNEP proteins are not as yet known, although
CC the neprilysin family of zinc endopeptidases play key roles in the
CC processing and/or metabolism or neuroprotection and peptide hormones. SNEP
CC nucleotides may be used as hybridisation probes for cDNA and genomic

CC DNA: to isolate full-length cDNAs and genomic clones encoding SNEPa,
 CC SNEPb or SNEPc; to isolate cDNA and genomic clones of SNEP homologues;
 CC as research reagents and material for the discovery of treatments and
 CC diagnostics for animal and human diseases; and for chromosome
 CC identification. The SNEP proteins may be used as immunogens to
 CC produce antibodies immunospecific for SNEPa, SNEPb or SNEPc. Such
 CC antibodies are used to isolate or identify clones expressing the
 CC protein, or to purify the proteins by affinity chromatography.
 CC SNEP proteins may also be used in screening for compounds which modulate
 CC SNEP endopeptidase activity, and to assess enzymatic cleavage of small
 CC molecule substrates in cells, cell-free preparations, chemical libraries
 CC and product mixtures. The SNEP proteins (as vaccine compositions),
 CC SNEP nucleotides, and SNEP activators or inhibitors may be used
 CC to treat acute and chronic renal insufficiency, renal and hepatic
 CC ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as
 CC well as cardiovascular, neuronal, pancreatic, prostatic, renal,
 CC respiratory or hepatic diseases. They may also be used in modulating
 CC peptide activation and/or degradation in the brain or kidney or in
 CC another organ, or to diagnose or treat any disorder related to abnormal
 CC expression of SNEPa, SNEPb or SNEPc. The present sequence represents
 CC SNEPb.
 XX
 SQ Sequence 753 AA;

Query Match 97.9%; Score 651; DB 22; Length 753;
 Best Local Similarity 100.0%; Pred. No. 6.7e-64;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHEITHGFDGNGRFDKNGNMWNSFSTQHFRQSECMYQYGNYSWDLADEQNVNGF 60
 |||||
 Db 586 gheithgfdgngfrfdkngnmmdwswnfstqhrqsecmlyqygnyswldadeqnvngf 645
 |||||
 Qy 61 NTLGENIADNGGVRQAYKAYLKWMAEGGKQDQOLPGLDLTHEQLFFINYAQVWCG 114
 |||||
 Db 646 ntlgeniadnggvrqaykaylkwmaegkgdqglpdltheqlffinyaqvwcg 699

RESULT 5
 AAB60563
 ID AAB60563 standard; Protein: 762 AA.
 AC AAB60563;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE Human neprilysin-like membrane metalloproteinase SNEPc.
 XX
 KW Human; SNEPc: neprilysin-like membrane metalloproteinase;
 KW splice variant; alternative splicing; zinc endopeptidase family;
 KW neuropeptide; peptide hormone; processing; metabolism; vaccine;
 KW drug screening; renal insufficiency; hepatic disease; ischaemia; pain;
 KW hypertension; cancer; inflammation; cardiovascular disease;
 KW neuronal disease; pancreatic disease; prostatic disease;
 KW respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic;
 KW cerebroprotective; hypotensive; cytostatic; antiinflammatory;
 KW cardiovascular; hepatotropic.
 XX
 OS Homo sapiens.
 XX
 PN EP1069188-A1.
 XX
 PD 17-JAN-2001.
 XX
 PF 15-JUL-1999; 99EP-0401767.
 XX
 PR 15-JUL-1999; 99EP-0401767.
 XX
 PA (SNFI) SANOFI-SYNTHELABO.
 XX
 PI Jagerschmidt A, Agnel M, Culouscou J;
 XX
 DR WPI; 2001-212582/22.

DR N-PSDB; AAF59661.
 XX
 PT New membrane-associated metalloproteinase SNEPa, SNEPb and SNEPc
 PT polypeptides and polynucleotides, useful for treating e.g. acute and
 PT chronic renal insufficiency, pain, stroke, cancer, inflammation, renal
 PT and hepatic ischaemia.
 XX
 PS Claim 11; Page 38-40; 72pp; English.

XX The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and
 CC the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like
 CC membrane metalloproteinases and are the products of alternative splicing.
 CC The substrate(s) for the SNEP proteins are not as yet known, although
 CC the neprilysin family of zinc endopeptidases play key roles in the
 CC processing and/or metabolism or neuropeptides and peptide hormones. SNEP
 CC nucleotides may be used as hybridisation probes for cDNA and genomic
 CC DNA; to isolate full-length cDNAs and genomic clones encoding SNEPa,
 CC SNEPb or SNEPc; to isolate cDNA and genomic clones of SNEP homologues;
 CC as research reagents and material for the discovery of treatments and
 CC diagnostics for animal and human diseases; and for chromosome
 CC identification. The SNEP proteins may be used as immunogens to
 CC produce antibodies immunospecific for SNEPa, SNEPb or SNEPc. Such
 CC antibodies are used to isolate or identify clones expressing the
 CC protein, or to purify the proteins by affinity chromatography.
 CC SNEP proteins may also be used in screening for compounds which modulate
 CC SNEP endopeptidase activity, and to assess enzymatic cleavage of small
 CC molecule substrates in cells, cell-free preparations, chemical libraries
 CC and product mixtures. The SNEP proteins (as vaccine compositions),
 CC SNEP nucleotides, and SNEP activators or inhibitors may be used
 CC to treat acute and chronic renal insufficiency, renal and hepatic
 CC ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as
 CC well as cardiovascular, neuronal, pancreatic, prostatic, renal,
 CC respiratory or hepatic diseases. They may also be used in modulating
 CC peptide activation and/or degradation in the brain or kidney or in
 CC another organ, or to diagnose or treat any disorder related to abnormal
 CC expression of SNEPa, SNEPb or SNEPc. The present sequence represents
 CC SNEPc.

XX Sequence 762 AA;

Query Match 97.9%; Score 651; DB 22; Length 762;
 Best Local Similarity 100.0%; Pred. No. 6.8e-64;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHEITHGFDGNGRFDKNGNMWNSFSTQHFRQSECMYQYGNYSWDLADEQNVNGF 60
 |||||
 Db 595 gheithgfdgngfrfdkngnmmdwswnfstqhrqsecmlyqygnyswldadeqnvngf 654
 |||||
 Qy 61 NTLGENIADNGGVRQAYKAYLKWMAEGGKQDQOLPGLDLTHEQLFFINYAQVWCG 114
 |||||
 Db 655 ntlgeniadnggvrqaykaylkwmaegkgdqglpdltheqlffinyaqvwcg 708

RESULT 6
 AAB08131
 ID AAB08131 standard; Protein: 770 AA.
 AC AAB08131;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE A human neutral endopeptidase metalloproteinase-like enzyme NL-2.
 XX
 KW Neprilysin; neutral endopeptidase metalloproteinase-like enzyme;
 KW NEP-like enzyme; protein production; protein secretion;
 KW neurological disease; Alzheimer's disease; pain; psychiatric disorder;
 KW fertility; bone disease; abnormal phosphate metabolism.
 XX
 OS Homo sapiens.
 XX
 PN WO2000/47750-A2.

PD 17-AUG-2000.
 XX
 PF 11-FEB-2000; 2000WO-CA00147.
 XX
 PR 11-FEB-1999; 99CA-2260376.
 XX
 PA (UYMO-) UNIV MONTREAL.
 XX
 PI Desgroseillers L, Boileau G;
 XX
 XX WPI; 2000-549148/50.
 DR N-PSDB; AAA63764.
 XX
 XX Novel neutral endopeptidase-like metalloproteinase polypeptides and
 PT polynucleotides, used to screen for related sequences and enzyme
 PT inhibitors, used for the treatment of NL-3 related bone disorders
 XX
 PS Claim 3; Fig 4; 59pp; English.
 XX
 XX The present sequence represents a human neutral endopeptidase
 CC metalloproteinase-like enzyme, designated NL-2. The specification
 CC also describes NL-1 and NL-3. The NL enzymes are used to test for
 CC specific inhibitors. The N-terminal region of the enzymes can be used
 CC to promote production and secretion of foreign proteins and active
 CC biopeptides, using chimeric constructs containing the foreign protein
 CC downstream from and in phase with the N-terminal region. The NL enzymes
 CC have been localised to the brain, and may be useful in the
 CC treatment of neurological diseases such as Alzheimer's disease, pain,
 CC and psychiatric disorders. NL enzymes have also been localised to the
 CC testis and ovaries, and may be used to control fertility. They have
 CC also been localised to bones, and may be used to treat bone diseases,
 CC and abnormal phosphate metabolisms related to improper peptide
 CC processing by the NL-3 enzyme.
 XX
 SQ Sequence 770 AA;

Query Match 97.9%; Score 651; DB 21; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.9e-64;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHEITHGFDNGRNFDPKNGMMWNSFSTQHFREQSECMYGYGYNSWDLADQNVNGF 60
 DB 603 gheithgfdngnrfndkngmmwdsntstghfrqsecmivgygynswdladqnvngf 662
 OY 61 NTLGENIADNGGVRQAYKAYLKWMAEGGKDDQLPGLDLTHEQLFFINYAQVWCG 114
 DB 663 ntlgeniadnggvrqaykaylkwmaeggdqqlpglditheqlffinyaqvwcg 716

RESULT 7
 AAB83841
 ID AAB83841 standard; Protein: 779 AA.
 XX
 AC AAB83841;
 XX
 XX 23-JUL-2001 (first entry)
 DT
 XX Amino acid sequence of a human metalloproteinase enzyme IGS5.
 DE
 XX Metalloproteinase; IGS5; infection; pain; cancer; diabetes; obesity;
 KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis;
 KW angina pectoris; myocardial infarction; stroke; ulcer; allergy;
 KW benign prostatic hypertrophy; migraine; psychotic disorder;
 KW neurological disorder; autism; multiple sclerosis; Alzheimer's disease;
 KW neurodegenerative disease; sleep disorder; epilepsy; kidney disease;
 KW cardiovascular disease; arteriosclerosis; cerebrovasospasm;
 KW subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
 KW peripheral vascular disease; Raynaud's disease; motility disorder;
 KW gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
 KW inflammation; chemotherapy induced injury; tumour invasion;
 KW immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;

KW severe mental retardation; dyskinesia; Huntington's disease;
 KW Gillies de-la Tourette's syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200136610-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-EP11532.
 XX
 PR 19-NOV-1999; 99EP-0203862.
 PR 19-NOV-1999; 99NL-1013616.
 PR 31-MAY-2000; 2000EP-0201937.
 PR 31-MAY-2000; 2000NL-1013556.
 XX
 PA (SOLV) SOLVAY PHARM BV.
 XX
 PI Deleersnijder W, Wiegers R, Weske M;
 DR WPI; 2001-343815/36.
 DR N-PSDB; AAF89738.
 XX
 XX New IGS5 polypeptides useful for treating infections, pain, cancer,
 PT diabetes, obesity, anorexia, bulimia, asthma, schizophrenia,
 PT hypertension, urinary retention and Parkinson's disease
 XX
 PS Claim 3; Page 8; 115pp; English.
 XX
 XX The present sequence represents a human metalloproteinase enzyme designated
 CC IGS5. IGS5 polynucleotides and polypeptides are useful for treating
 CC infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma,
 CC Parkinson's disease, acute heart failure, hypotension, hypertension,
 CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
 CC stroke, ulcers, allergies, benign prostatic hypertrophy, migraine,
 CC psychotic and neurological disorders, autism, multiple sclerosis,
 CC Alzheimer's disease, and other neurodegenerative diseases; sleep
 CC disorder, epilepsy, cardiovascular diseases, arteriosclerosis,
 CC cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral
 CC infarction, peripheral vascular disease, Raynaud's disease, kidney
 CC diseases, gastrointestinal disorders, motility disorders and conditions
 CC of delayed gastric emptying, post-operative or diabetic gastroparesis,
 CC diarrhoea, inflammations, chemotherapy induced injury, tumour invasion,
 CC immune disorders, arthritis, endotoxin shock, sepsis, complications of
 CC diabetes mellitus, and severe mental retardation and dyskinesias, such
 CC as Huntington's disease or Gilles de la Tourette's syndrome.
 XX
 SQ Sequence 779 AA;

Query Match 97.9%; Score 651; DB 22; Length 779;
 Best Local Similarity 100.0%; Pred. No. 7e-64;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHEITHGFDNGRNFDPKNGMMWNSFSTQHFREQSECMYGYGYNSWDLADQNVNGF 60
 DB 612 gheithgfdngnrfndkngmmwdsntstghfrqsecmivgygynswdladqnvngf 671
 OY 61 NTLGENIADNGGVRQAYKAYLKWMAEGGKDDQLPGLDLTHEQLFFINYAQVWCG 114
 DB 672 ntlgeniadnggvrqaykaylkwmaeggdqqlpglditheqlffinyaqvwcg 725

RESULT 8
 AAB60561
 ID AAB60561 standard; Protein: 779 AA.
 XX
 AC AAB60561;
 XX
 XX 27-APR-2001 (first entry)
 DT
 XX Human neprilysin-like membrane metalloproteinase SNEPa.

Human; SNEPa; neprilysin-like membrane metalloproteinase;
 splice variant; alternative splicing; zinc endopeptidase family;
 neuropeptide; peptide hormone; processing; metabolism; vaccine;
 drug screening; renal insufficiency; hepatic disease; ischaemia; pain;
 hypertension; cancer; inflammation; cardiovascular disease;
 neuronal disease; pancreatic disease; prostatic disease;
 respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic;
 cerebroprotective; hypotensive; cytostatic; antiinflammatory;
 cardiovascular; hepatotropic.

OS Homo sapiens.
 XX
 XX EP1069188-A1.
 XX
 XX PD 17-JAN-2001.
 XX
 XX PF 15-JUL-1999; 99EP-0401767.
 XX
 XX PR 15-JUL-1999; 99EP-0401767.
 XX
 XX PA (SNFI) SANOFI-SYNTHELABO.
 XX
 XX PI Jagerschmidt A, Agnel M, Culouscou J;
 XX
 XX DR WPI; 2001-212582/22.
 XX
 XX DR N-PSDB; AAF59659.
 XX
 XX PT New membrane-associated metalloproteinase SNEPa, SNEPb and SNEPc
 PT polypeptides and polynucleotides, useful for treating e.g. acute and
 PT chronic renal insufficiency, pain, stroke, cancer, inflammation, renal
 PT and hepatic ischemia
 XX
 XX PS Claim 11; Page 28-30; 72pp; English.
 XX
 XX CC The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and
 CC the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like
 CC membrane metalloproteinases and are the products of alternative splicing.
 CC The substrate(s) for the SNEP proteins are not as yet known, although
 CC the neprilysin family of zinc endopeptidases play key roles in the
 CC processing and/or metabolism of neuropeptides and peptide hormones. SNEP
 CC nucleotides may be used as hybridisation probes for cDNA and genomic
 CC DNA; to isolate full-length cDNAs and genomic clones encoding SNEPa,
 CC SNEPb or SNEPc; to isolate cDNA and genomic clones of SNEP homologues;
 CC as research reagents and material for the discovery of treatments and
 CC diagnostics for animal and human diseases; and for chromosome
 CC identification. The SNEP proteins may be used as immunogens to
 CC produce antibodies immunospecific for SNEPa, SNEPb or SNEPc. Such
 CC antibodies are used to isolate or identify clones expressing the
 CC protein, or to purify the proteins by affinity chromatography.
 CC SNEP proteins may also be used in screening for compounds which modulate
 CC SNEP endopeptidase activity, and to assess enzymatic cleavage of small
 CC molecule substrates in cells, cell-free preparations, chemical libraries
 CC and product mixtures. The SNEP proteins (as vaccine compositions),
 CC SNEP nucleotides, and SNEP activators or inhibitors may be used
 CC to treat acute and chronic renal-insufficiency, renal and hepatic
 CC ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as
 CC well as cardiovascular, neuronal, pancreatic, prostatic, renal,
 CC respiratory or hepatic diseases. They may also be used in modulating
 CC peptide activation and/or degradation in the brain or kidney or in
 CC another organ, or to diagnose or treat any disorder related to abnormal
 CC expression of SNEPa, SNEPb or SNEPc. The present sequence represents
 CC SNEPa.
 XX
 XX SQ Sequence 779 AA;

Query Match 97.9%; Score 651; DB 22; Length 779;
 Best Local Similarity 100.0%; Pred. No. 7e-64;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHEITHGFDNNGNFKNGNMMDWSNFSTQHFRQSECMYQYGNYSWDLADEQNVNGF 60
 :|||||
 Db 612 gheithgfdnngnfdknngnmmdwsnfstqhfrqsecmiyqygnyswldadeqnvngf 671
 :|||||

QY 61 NTLGENIADNGVROAYKAYLKWMAEGGKDDQLPGLDLTHEQLFFINYAQVWCG 114
 :|||||
 Db 672 nctigeniadnggvrraykaylkwmaeggkddqlpgldltheqffinyaqvwcg 725
 :|||||

RESULT 9
 AAB08130
 ID AAB08130 standard; Protein; 765 AA.
 XX
 XX AC AAB08130;
 XX
 XX DT 04-DEC-2000 (first entry)
 XX
 XX DE A murine neutral endopeptidase metalloproteinase-like enzyme NL-1.
 XX
 XX KW Neprilysin; neutral endopeptidase metalloproteinase-like enzyme;
 KW NEP-like enzyme; protein production; protein secretion;
 KW neurological disease; Alzheimer's disease; pain; psychiatric disorder;
 KW fertility; bone disease; abnormal phosphate metabolism.
 XX
 XX OS Mus sp.
 XX
 XX PN WO200047750-A2.
 XX
 XX PD 17-AUG-2000.
 XX
 XX PF 11-FEB-2000; 2000WO-CA00147.
 XX
 XX PR 11-FEB-1999; 99CA-2260376.
 XX
 XX PA (UYMO-) UNIV MONTREAL.
 XX
 XX PI Desgroseillers L, Boileau G;
 XX
 XX DR WPI; 2000-549148/50.
 XX
 XX DR N-PSDB; AAA63763.
 XX
 XX PT Novel neutral endopeptidase-like metalloproteinase polypeptides and
 PT polynucleotides, used to screen for related sequences and enzyme
 PT inhibitors, used for the treatment of NL-3 related bone disorders -
 XX
 XX PS Claim 2; Fig 3; 59pp; English.
 XX
 XX CC The present sequence represents a murine neutral endopeptidase
 CC metalloproteinase-like enzyme, designated NL-1. The specification
 CC also describes NL-2 and NL-3. The NL enzymes are used to test for
 CC specific inhibitors. The N-terminal region of the enzymes can be used
 CC to promote production and secretion of foreign proteins and active
 CC biopeptides, using chimeric constructs containing the foreign protein
 CC downstream from and in phase with the N-terminal region. The NL enzymes
 CC are have been localised to the brain, and may be useful in the
 CC treatment of neurological diseases such as Alzheimer's disease, pain,
 CC and psychiatric disorders. NL enzymes have also been localised to the
 CC testis and ovaries, and may be used to control fertility. They have
 CC also been localised to bones, and may be used to treat bone diseases,
 CC and abnormal phosphate metabolisms related to improper peptide
 CC processing by the NL-3 enzyme.
 XX
 XX SQ Sequence 765 AA;

Query Match 87.4%; Score 581; DB 21; Length 765;
 Best Local Similarity 85.1%; Pred. No. 4.4e-56;
 Matches 97; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEITHGFDNNGNFKNGNMMDWSNFSTQHFRQSECMYQYGNYSWDLADEQNVNGF 60
 :|||||
 Db 598 gheithgfdnngnfdknngnmmdwsnfstqhfrqsecmiyqygnyswldadeqnvngf 657
 :|||||

QY 61 NTLGENIADNGVROAYKAYLKWMAEGGKDDQLPGLDLTHEQLFFINYAQVWCG 114
 :|||||
 Db 658 stligeniadnggvrraykaylrlwladggkddqrlpglnltyaqffinyaqvwcg 711
 :|||||

RESULT 10

AA44177
ID AAY44177 standard; Protein; 774 AA.

XX AC
XX AAY44177;

XX DT 01-FEB-2000 (first entry)

XX DE Rat membrane metalloprotease NEPII protein.

XX KW Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation;
XX KW neuron; hormone; peptide messenger; inhibitor; detection; disorder;
XX KW cardiovascular disease; neurodegenerative disease; growth disorder;
XX KW hypothalamic-hypophyseal axis; endocrine disorder.

XX OS Rattus rattus.

XX PN FR2777291-A1.

XX PD 15-OCT-1999.

XX PF 08-APR-1998; 98FR-0004389.

XX PR 08-APR-1998; 98FR-0004389.

XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX PI Oulmet T, Gros C, Haret C, Bonhomme MC, Facchinetti P;
XX PI Schwartz JC;

XX DR WPI; 1999-593429/51.

XX DR N-PSDB; AA228810.

XX PT New membrane metalloprotease NEPII, involved in proteolysis of
XX PT neuronal and hormonal peptides, used to screen for inhibitors,
XX PT potentially useful for treating e.g. cardiovascular disease -

XX PS Claim 1; Page 12-16; 29pp; French.

XX CC This sequence represents the rat membrane metalloprotease designated
XX CC neprilysine II (NEPII), which is involved in (in)activation of neuronal
XX CC and hormonal peptide messengers. NEPII is used to screen for specific
XX CC substrates (used to detect NEPII in cells and tissues) or inhibitors,
XX CC which can also be used to detect NEPII or for treatment of disorders
XX CC related to peptidergic signalling in which NEPII is involved, e.g.
XX CC cardiovascular or neurodegenerative diseases; growth disorders of
XX CC endocrine origin; disturbances of the hypothalamic-hypophyseal axis
XX CC or endocrine disorders.

XX SQ Sequence 774 AA;

Query Match 86.9%; Score 578; DB 20; Length 774;

Best Local Similarity 85.1%; Pred. No. 9.7e-56;

Matches 97; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

OY 1 GHEITHGFDNGRNFDKNGNMWWSNFSQHFREQSECMYQYGNYSWDLADQNNGVF 60
Db 607 gheithgfdngnfrnfdkngnmldwsnfsarhfrqscmlygysnfweladnqnngvf 666

OY 61 NTGENTADNGGVRQAYKAYLKWMAEGGKDOQLPGLDLTHEQLFFINVAQVWCG 114

Db 667 stlgeniadnggvrqaykaylqlwlaeggrdrlpglnltyaqilffinyaqvwcg 720

RESULT 11

AAP82940

ID AAP82940 standard; protein; 750 AA.

XX AC

XX AAP82940;

XX

DT 23-NOV-1990 (first entry)

XX DE Atrial natriuretic polypeptide binding polypeptide.

XX KW Diuretic; atrium cardis; atrial natriuretic peptide binding;
XX KW hypotensive action.

XX PN JP63079598-A.

XX PD 09-APR-1988.

XX PF 22-SEP-1986; 86JP-0222192.

XX PR 22-SEP-1986; 86JP-0222192.

XX PA (SUNR) SUNTORY LTD.

XX WIPI; 1988-137132/20.

XX DR N-PSDB; AAN81690.

XX PT Novel polypeptide, with diuretic action - is obtd. from atrium cardis
XX PT of mammals showing specific bond to atrial natriuretic polypeptide
XX PT and gene codinh it.

XX PS Disclosure; ; p; Japanese.

XX CC Peptide specifically binds to atrial natriuretic polypeptide (ANP)
XX CC and has diuretic (partic. natriuretic) and hypotensive action.
XX CC See also AAN81690-93 and AAP81282-P81309.

XX SQ Sequence 750 AA;

Query Match 70.8%; Score 471; DB 9; Length 750;

Best Local Similarity 66.7%; Pred. No. 8.2e-44;

Matches 76; Conservative 24; Mismatches 14; Indels 0; Gaps 0;

OY 1 GHEITHGFDNGRNFDKNGNMWWSNFSQHFREQSECMYQYGNYSWDLADQNNGVF 60
Db 583 gheithgfdngnfrnfdkngnmldwsgtqannfkqsgcmvyqygnfswdlaggghlngi 642

OY 61 NTGENTADNGGVRQAYKAYLKWMAEGGKDOQLPGLDLTHEQLFFINVAQVWCG 114

Db 643 ntigeniadnggvgayrayqayqnyvkngeekllpgldlnhkhqlfflnfaqvwcg 696

RESULT 12

AAE07916

ID AAE07916 standard; Protein; 743 AA.

XX AC AAE07916;

XX DT 01-NOV-2001 (first entry)

XX DE Human neutral endopeptidase (NEP) protein.

XX KW Human; female sexual dysfunction; FSD; female sexual arousal dysfunction;
XX KW FSAD; neuropeptide Y; NPY; gynaecological; neutral endopeptidase; NEP;
XX KW enkephalinase; vasoactive intestinal peptide; VIP.

XX OS Homo sapiens.

XX PN EP1097718-A1.

XX PD 09-MAY-2001.

XX PF 03-NOV-2000; 2000EP-0309720.

XX PR 08-NOV-1999; 99GB-0026437.

XX PR 18-FEB-2000; 2000GB-0004021.

XX PR 26-MAY-2000; 2000GB-0013001.

XX PR 05-JUL-2000; 2000GB-0016563.

XX PR 12-JUL-2000; 2000GB-0017141.

XX (PFIZ) PRIZER LTD.
PA (PFIZ) PRIZER INC.
XX
XX Maw GN, Wayman CP;
XX WPI; 2001-319199/34.
DR N-PSDB; AAD14514.
XX
PT Treating females suffering from female sexual dysfunction, preferably
PT female sexual arousal dysfunction using a neuropeptide Y inhibitor that
PT potentiates cAMP in female genitalia
XX
XX Claim 1; Page 112-115; 165pp; English.
XX
CC The patent discloses a method for the treatment of a female suffering
CC from female sexual dysfunction (FSD), preferably female sexual arousal
CC dysfunction (FSAD) by the use of an agent which is an inhibitor of
CC neuropeptide Y (NPY). The agent is capable of potentiating cAMP which
CC enhances female genital (e.g. vaginal or clitoral) blood flow in the
CC sexual genitalia of the female and is optionally admixed with a diluent
CC carrier or excipient. The method restores a normal sexual arousal
CC response namely, increased blood flow leading to vaginal, clitoral
CC lubrication via plasma transduction, increased vaginal compliance
CC and increased genital (e.g. vaginal and clitoral) sensitivity. The
CC method is used for treating a female suffering from FSD preferably
CC FSAD. The present sequence is neutral endopeptidase (NEP) protein
CC from human (E.C. 3.4.24.11). NEP is also known as enkephalinase. It
CC metabolises vasoactive intestinal peptide (VIP) and hence terminates VIP-
CC mediated biological activity. NEP inhibitors potentiate the endogenous
CC vasorelaxant effect of VIP released during arousal. They enhance pelvic
CC nerve stimulated increase in vaginal and clitoral blood flow.
XX
SQ Sequence 743 AA;

Query Match 70.5%; Score 469; DB 22; Length 743;
Best Local Similarity 66.7%; Pred. No. 1.3e-43;
Matches 76; Conservative 24; Mismatches 14; Indels 0; Gaps 0;
QY 1 GHEITHGFDNGRNFKNMMDWSNFTQHFQSECMYQYGNYSWDLADEQNVNGF 60
Db 576 gheithgfdnggrnfnkdgldvdtqqsasnfkqscmqvgygnfswdlaggqhngi 635
QY 61 NTLGENIADNGVGRQAYKAYLKWMAEGGKDDQLPGLDLTHEQLFFINYAQVWCG 114
Db 636 ntlgeniadngvgayrayqnyikngeekllpgldlnhkhgllfnfagvwcg 689

RESULT 13
AAE07952
ID AAE07952 standard; Protein; 743 AA.
XX
AC AAE07952;
XX
DT 01-NOV-2001 (first entry)
XX
DE Human neutral endopeptidase (NEP).
XX
KW Human; female sexual dysfunction; FSD; female sexual arousal dysfunction;
KW FSAD; neutral endopeptidase inhibitor; I.NEP; enkephalinase;
KW gynaecological; endopeptidase-2.
XX
OS Homo sapiens.
XX
PN EP1097719-A1.
XX
PD 09-MAY-2001.
XX
PF 03-NOV-2000; 2000EP-0309722.
XX
PR 08-NOV-1999; 99GB-0026437.

PR 18-FEB-2000; 2000GB-0004021.
PR 26-MAY-2000; 2000GB-0013001.
PR 05-JUL-2000; 2000GB-0016563.
PR 12-JUL-2000; 2000GB-0017141.
XX
PA (PFIZ) PRIZER LTD.
PA (PFIZ) PRIZER INC.
XX
PI Maw GN, Wayman CP;
XX
DR WPI; 2001-309880/33.
DR N-PSDB; AAD14524.
XX
PT Treating females suffering from female sexual dysfunction, preferably
PT female sexual arousal dysfunction using a neutral endopeptidase
PT inhibitor that potentiates cAMP in female genitalia
XX
XX Claim 1; Page 90; 124pp; English.
XX
CC The present invention relates to a method for treating female sexual
CC dysfunction (FSD), preferably female sexual arousal dysfunction (FSAD).
CC The method comprising using an agent, an inhibitor of neutral
CC endopeptidase (NEP) EC 3.4.24.11 or I.NEP, which is capable of
CC potentiating cAMP (which enhances female genital blood flow) in the
CC sexual genitalia of the females. NEP is also known as enkephalinase or
CC endopeptidase-2. The agent is optionally admixed with a diluent, carrier
CC or excipient. The method restores a normal sexual arousal response,
CC particularly increased blood flow leading to vaginal, clitoral and
CC labial engorgement. This will result in increased vaginal lubrication
CC via plasma transduction, increased vaginal compliance and increased
CC genital (e.g. vaginal and clitoral) sensitivity. The present sequence is
CC human neutral endopeptidase (NEP).
XX
SQ Sequence 743 AA;

Query Match 70.5%; Score 469; DB 22; Length 743;
Best Local Similarity 66.7%; Pred. No. 1.3e-43;
Matches 76; Conservative 24; Mismatches 14; Indels 0; Gaps 0;
QY 1 GHEITHGFDNGRNFKNMMDWSNFTQHFQSECMYQYGNYSWDLADEQNVNGF 60
Db 576 gheithgfdnggrnfnkdgldvdtqqsasnfkqscmqvgygnfswdlaggqhngi 635
QY 61 NTLGENIADNGVGRQAYKAYLKWMAEGGKDDQLPGLDLTHEQLFFINYAQVWCG 114
Db 636 ntlgeniadngvgayrayqnyikngeekllpgldlnhkhgllfnfagvwcg 689

RESULT 14
AAB85104
ID AAB85104 standard; Protein; 743 AA.
XX
AC AAB85104;
XX
DT 22-AUG-2001 (first entry)
XX
DE Human enkephalinase (EC 3.4.24.11).
XX
KW Female sexual dysfunction; FSD; female sexual arousal disorder; FSAD;
KW genital; vaginal; clitoral; blood flow; cAMP; phosphodiesterase; PDE;
KW CGMP; medicament; human; enkephalinase; neutral endopeptidase; NEP.
XX
OS Homo sapiens.
XX
PN EP1097706-A1.
XX
PD 09-MAY-2001.
XX
PF 03-NOV-2000; 2000EP-0309718.
XX
PR 08-NOV-1999; 99GB-0026437.
PR 18-FEB-2000; 2000GB-0004021.

PR 26-MAY-2000; 2000GB-0013001.
 PR 05-JUL-2000; 2000GB-0016563.
 PR 12-JUL-2000; 2000GB-0017141.
 XX
 PA (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX
 PI Maw GN, Wayman CP;
 XX
 XX
 DR WPI: 2001-383216/41.
 DR N-PSDB; AAF84073.

XX Novel pharmaceutical composition for treating female sexual
 PT dysfunction, preferably female sexual arousal disorder, comprising an
 PT agent capable of potentiating CAMP in the sexual genitalia of the
 PT female
 XX

PS Disclosure; Page 95; 132pp; English.

XX The invention provides a pharmaceutical composition for treating female
 CC sexual dysfunction (FSD), preferably female sexual arousal disorder
 CC (FSAD), or enhancing female genital (e.g. vaginal or clitoral) blood flow
 CC in a female. The composition comprises an agent capable of potentiating
 CC CAMP in the sexual genitalia of the female. The agent is an inhibitor
 CC (1:PDE) of phosphodiesterase (PDE), which hydrolyzes CAMP (optionally
 CC cGMP). The agent is useful in the manufacture of a medicament for the
 CC treatment of FSD, preferably FSAD, by potentiating CAMP in the sexual
 CC genitalia. It is also useful in the manufacture of a medicament for
 CC enhancing female genital (e.g., vaginal or clitoral) blood flow. The
 CC present sequence represents a human enkephalinase, a neutral
 CC endopeptidase (NEP) that can be used as an additional PCAMP target.
 XX

SQ Sequence 743 AA;

Query Match 70.5%; Score 469; DB 22; Length 743;
 Best Local Similarity 66.7%; Pred. No. 1.3e-43;
 Matches 76; Conservative 24; Mismatches 14; Indels 0; Gaps 0;

Oy 1 GHEITHGDDNGRNFDRKNGNMWNSFSTQHFREQSECMYQYGNYSWDLADQNNGVP 60
 Db 576 gheithgddnggrnfrnkdgdlvwtgqsasnfkeqscmvyqygnfswdlaggghlngi 635
 Oy 61 NTLGENIADNGGVROAYKAYLKWMAEGGKDOQLPCLDLTTHEOLFETINYAQVWCG 114
 Db 636 ntlgeniadngglgqayrayqnyikngeekilpdlhnhkqlflnfaqvwcg 689

RESULT 15
 AAB85115
 ID AAB85115 standard; Protein: 743 AA.

XX AAB85115;

XX 22-AUG-2001 (first entry)

XX Human enkephalinase (EC 3.4.24.11).

XX Female sexual dysfunction; FSD; female sexual arousal disorder; FSAD;
 KW genital; vaginal; clitoral; blood flow; CAMP; phosphodiesterase; PDE;
 KW cGMP; medicament; human; enkephalinase; neutral endopeptidase; NEP.

XX Homo sapiens.

XX EPI097707-AL.

XX 09-MAY-2001.

XX 03-NOV-2000; 2000EP-0309719.

XX 08-NOV-1999; 99GB-0026437.

XX 18-FEB-2000; 2000GB-0004021.

XX 26-MAY-2000; 2000GB-0013001.

PR 05-JUL-2000; 2000GB-0016563.
 PR 12-JUL-2000; 2000GB-0017141.
 XX
 PA (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX
 PI Maw GN, Wayman CP;
 XX
 XX
 DR WPI: 2001-383217/41.
 DR N-PSDB; AAF84083.

XX Novel pharmaceutical composition for treating female sexual
 PT dysfunction, preferably female sexual arousal disorder, comprising an
 PT agent capable of potentiating CAMP in the sexual genitalia of the
 PT female
 XX

PS Disclosure; Page 98; 135pp; English.

XX The invention provides a pharmaceutical composition for treating female
 CC sexual dysfunction (FSD), preferably female sexual arousal disorder
 CC (FSAD), or enhancing female genital (e.g. vaginal or clitoral) blood flow
 CC in a female. The composition comprises an agent capable of potentiating
 CC CAMP in the sexual genitalia of the female. The agent is an inhibitor
 CC (1:PDE) of phosphodiesterase (PDE), which hydrolyzes CAMP (optionally
 CC cGMP). The agent is useful in the manufacture of a medicament for the
 CC treatment of FSD, preferably FSAD, by potentiating CAMP in the sexual
 CC genitalia. It is also useful in the manufacture of a medicament for
 CC enhancing female genital (e.g., vaginal or clitoral) blood flow. The
 CC present sequence represents a human enkephalinase, a neutral
 CC endopeptidase (NEP) that can be used as an additional PCAMP target.
 XX

SQ Sequence 743 AA;

Query Match 70.5%; Score 469; DB 22; Length 743;
 Best Local Similarity 66.7%; Pred. No. 1.3e-43;
 Matches 76; Conservative 24; Mismatches 14; Indels 0; Gaps 0;

Oy 1 GHEITHGDDNGRNFDRKNGNMWNSFSTQHFREQSECMYQYGNYSWDLADQNNGVP 60
 Db 576 gheithgddnggrnfrnkdgdlvwtgqsasnfkeqscmvyqygnfswdlaggghlngi 635
 Oy 61 NTLGENIADNGGVROAYKAYLKWMAEGGKDOQLPCLDLTTHEOLFETINYAQVWCG 114
 Db 636 ntlgeniadngglgqayrayqnyikngeekilpdlhnhkqlflnfaqvwcg 689

Search completed: October 3, 2002, 11:07:38
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gb_esc12:BE245100	+ 373.00	819.20	2.2e-36	549	! BE245100 TCBAPI9D2535 Pediatric
gb_esc12:W89492	+ 372.50	818.99	2.3e-36	501	! W89492 mf70d09.r1 Soares mouse
gb_esc12:BI869244	+ 367.50	801.33	2.2e-35	968	! BI869244 603396112F1 NIH_MGC_90
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BASE COUNT
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 High quality sequence stop: 459.
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 /clone="IMAGE:313540"
 /clone_lib="Soares mouse p3NMF19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /note="vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGGCCGTCATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
 BASE COUNT 218 a 142 c 163 g 177 t
 ORIGIN

alignment_scores:
 Quality: 437.00 Length: 114
 Ratio: 4.243 Gaps: 0
 Percent Similarity: 90.351 Percent Identity: 63.158

alignment_block:
 US-09-647-780A-4 x AI325325

Align seg 1/1 to: AI325325 from: 1 to: 705

1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAsp 17
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 17 sAsnGlyAsnMetMetAspTrpSerAsnPheSerThrGlnHisPheA 34
 245 AGATGGAGACCTCGTTGACTGGTGGACGAGCAGTCGCAATAATTTA 294
 34 rGluGlnSerGluCysMetIleTyrlGlnTyrlGlyAsnTyrlSerTrpAsp 50
 295 AAGACCAATCCAGTGATGGTATACCACTATGGAAACTTTTCTCTGTGAC 344
 51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsn 67
 345 CTAGCAGGTGGACACATCTCAATGGAATTAATACACTAGGAGAAACAT 394
 67 eAlaAspAsnGlyValArgGlnAlaTyrlValAlaTyrlLeuLysTrp 84
 395 TCGTGTATATGAGGTATTGGCAACATACAGAGCCTATCAGAAATTATG 444
 84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
 445 TTAAGAAGATGGTGAAGAAAATTAATCTCCTGGACTTGACCTCAATCAC 494
 101 GluGlnLeuPhePheIleAsnTyrlAlaGlnValTrpCysGly 114
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seq_documentation_block:

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 DEFINITION '602271182F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4359141 5',
 mRNA sequence.
 ACCESSION BF968576
 VERSION BF968576.1 GI:12335791

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 Quality: 449.00 Length: 114
 Ratio: 4.317 Gaps: 0
 Percent Similarity: 91.228 Percent Identity: 63.158
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 218 GGACAGAAATCACCCATGGCTTCGATGACATGGCAGAAATTTAACA 267
 17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
 268 GGATGGAGACCTTGTGACTGGTGGACTCAACAGCTCTGCAATAATTTTA 317
 34 rGluGlnSerGluCysMetIleTyrlGlnTyrlGlyAsnTyrlSerTrpAsp 50
 318 AAGACCTATCCAGTGGATGGTACCATGATGGGAATCTTCTCTGGGAC 367
 51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsn 67
 368 CTAGCAATGGACAGCATCTCAATGGAAATTAATACACTGGGAGAAACAT 417
 67 eAlaAspAsnGlyValArgGlnAlaTyrlLysAlaTyrlLeuLysTrp 84
 418 TGCATGAATGGTGTATGGTCCCAAGCATACAGAGCCATCAAACTATG 467
 84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
 468 TTAAGAAGATGGTGAAGAAAATTAATCTTCTGGACTTGACCTAAATCAC 517
 101 GluGlnLeuPhePheIleAsnTyrlAlaGlnValTrpCysGly 114
 518 AGACACTGTCTTCTCGAATTTGCCCANNTGTGGTGTGGA 559

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 IMAGE:313540 5' similar to gb:J03779 NEPRILYSIN (HUMAN);, mRNA
 sequence.
 ACCESSION AI325325
 VERSION AI325325.1 GI:4059754
 KEYWORDS EST
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 705)
 REFERENCE
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:204156
 This read is a RESEQUENCE of a previously sequenced mouse clone

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 926)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9998 row: d column: 22
High quality sequence stop: 766.

FEATURES
source
1..926
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4359141"
/clone_lib="NIH_MGC_84"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
BASE COUNT 286 a 192 c 221 g 227 t
ORIGIN
|||||
alignment_scores
Quality: 428.00 Length: 112
Ratio: 4.076 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 65.179

alignment_block
US-09-647-780A-4 x BF968576
Align seg 1/1 to: BF968576 from: 1 to: 926
3 Glu1eThrHisGlyPheAspAsnGlyArgAsnPheAspLysAsnG1 19
|||||
2 GAATCACCCTGGCTTCGATGATCAATGGCAGAACTTTACAAAGATGG 51
19 yAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheArgGluG 36
|||||
52 AGACCTCGTTGACTGGTGGAGTCAACAGTGTGCAAGTAACCTTTAAGGAGC 101
36 lnSerGluCysMetIleTyrglnTyrglyAsnTyrsrTrpAspLeuAla 52
|||||
102 AATCCCAAGTCATGGTGTATCAGTATGGAACCTTTCTCGGAGCTGGCA 151
53 AspGluGlnAsnValAsnGlyPheAsnThrLeuGluAsnIleAlaAs 69
|||||
152 GGTGCAGACGACCTTAATGGAATTAATACACTGGGAGAAACAT GCTGA 200
69 pAsnGlyGlyValArgGlnAlaTyrlsAlaTyrlsLeuLysTrpMetAlag 86
|||||
201 TAATGGAGGCTTGTTCAGCATACAGAGCCCTATCAGAAATATATATAAA 250
86 luGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHisGluGln 102
|||||
251 AGAATGCGAGAAATAATCTCTCGACTTGACCTAAATACAAACAA 300
103 LeuPhePheIleAsnTyrlaGlnValTrpCysGly 114
|||||

301 CTATTTTCTTGAACCTTGCACAGGTGTGGTGTGGA 336
seq_name: gb_est:AW940129
seq_documentation_block:
LOCUS AW940129 899 bp mRNA linear EST 23-APR-2001
DEFINITION GH03315.3prime GH Drosophila melanogaster head pot2 Drosophila melanogaster cDNA clone GH03315 3' mRNA sequence.
ACCESSION AW940129
VERSION AW940129.1 GI:8115575
SOURCE EST
ORGANISM fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 899)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
TITLE BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Other_ESTRs: GH03315.5prime
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd., Berkeley, CA 94720, USA
Fax: 510 436 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. hit genomic AE003436: Drosophila melanogaster genomic scaffold 142000013386054 section 20 of 35, complete sequence.: 02/14/2001
Plate: GH.33 row: B column: 3
High quality sequence stop: 819.

FEATURES
source
1..899
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH03315"
/clone_lib="GH Drosophila melanogaster head pot2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/notes="Organ: head; Vector: pot2; Site: 1; EcoRI; Site: 2; XhoI; Sited fractionated cDNAs were directly ligated into pot2. Plasmid cDNA library."
BASE COUNT 213 a 223 c 240 g 221 t 2 others
ORIGIN
|||||
alignment_scores
Quality: 397.50 Length: 114
Ratio: 4.015 Gaps: 1
Percent Similarity: 86.842 Percent Identity: 59.649

alignment_block
US-09-647-780A-4 x AW940129/rev
Align seg 1/1 to reverse of: AW940129 from: 1 to: 899
1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAsp17
|||||
830 GCCACGAGATTACCCGAGTTCGACGACAGGCGCAGCTGCACAA 781
17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
|||||
780 GGAGGGCAACATGATGTCAGTGTGGAACAATGCCACCATCGAGGCTTTC 731
34 rgGluGlnSerGluCysMetIleTyrglnTyrglyAsnTyrsrTrpasp 50
|||||
730 CGCAACGCGACGAGCTGCATCGATCAGTACTCGCTACAAGATTAAAC 681

BASE COUNT 184 a 110 c 124 g 131 t 1 others
ORIGIN

alignment_scores:

Quality: 375.00 Length: 100
Ratio: 4.032 Gaps: 0
Percent Similarity: 93.000 Percent Identity: 65.000

alignment_block:

US-09-647-780A-4 x BE245519

Align seg 1/1 to: BE245519 from: 1 to: 550

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1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAsp 17
|||||
250 GGACAGAAATCACCCTGCTTCGATGCAATGCGAAGAACTTTAAACA 299
|||||

17 sAsnGlyAsnMetMetAspTrpSerAsnPheSerThrGlnHisPheA 34
|||||
300 AGATGGAGACCTCGTGTACTGGTGACACACAGCTGCAAGTAACCTTA 349
|||||

34 rgGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrp 50
|||||
350 AGGAGCAATCCAGTCGATGGTGTATCAGTATGGAACCTTTCTCTGGG 399
|||||

51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAs 67
|||||
400 CTGGCAGGTGGACAGCACCTTAATGGAATTAATACACTGGGAGAAAC 449
|||||

67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLys 84
|||||
450 TGCTGATATGAGAGCTCTGTGTCAGCATACAGACCTTATCAGAATT 499
|||||

84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThr 100
|||||
500 TTAAGAAGATGGCGAAGAAATTA.CTTCTGGACTTGACCTAAATCAC 548
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```

seq_name: gb_est2:B1692693

seq_documentation_block:

LOCUS B1692693 536 bp mRNA linear EST 18-SEP-2001
DEFINITION 60343357F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5370927 5',
mRNA sequence.

ACCESSION B1692693

VERSION B1692693.1 GI:15655322

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 536)

AUTHORS NTH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapsb-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1A11944 Row: b Column: 16

High quality sequence stop: 536.

Location/Qualifiers

1..536

/organism="Mus musculus"

/strain="FVB/N-3"

/db_xref="taxon:10090"

/clone="IMAGE:5370927"

/clone_lib="NCI_CGAP_Mam2"

FEATURES

Source

/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 99 a 162 c 156 g 119 t
ORIGIN

alignment_scores:

Quality: 373.50 Length: 116
Ratio: 3.851 Gaps: 1
Percent Similarity: 83.621 Percent Identity: 54.310

alignment_block:

US-09-647-780A-4 x B1692693/rev

Align seg 1/1 to reverse of: B1692693 from: 1 to: 536

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1 GlyHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAsp 17
|||||
419 GCCCAGCAGCTGACTCAGCTTCGATGATCAAGTCCGGAGTACGACA 370
|||||

17 sAsnGlyAsnMetMetAspTrpSerAsnPheSerThrGlnHisPheA 34
|||||
369 GGATGGAAACCTTCGACCCTGGTGGGAAGACCTGCTCCGTGGAGCGCTTCA 320
|||||

34 rgGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrp 50
|||||
319 ACCAGCAGACGAGTGCATGGTGCACATAACAGCAACTACAGC..... 276
|||||

51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAs 67
|||||
275 ...GTGAACGGGGAGCCCGCTGAACGCTGCACACACCCCTCGGGGAGAACAT 229
|||||

67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLys 84
|||||
228 TCCCGCAACGGGGGACTCAAGCGGCGCTACCGGGCGTACCAGAACTGGG 179
|||||

84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThr 100
|||||
178 TAAAGAAGACGAGCTGAGCAGATGCTGCCACCCCTGGTCTCACCAGC 129
|||||

101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGlyCys 116
|||||
128 AACCACTCTTCTCTCCTAGGATTTCACAGAGTCTGTGTCTCTGTCCGC 81
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seq_name: gb_est2:BE245100

seq_documentation_block:

LOCUS BE245100 549 bp mRNA linear EST 03-OCT-2001
DEFINITION TCBAPID2535 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP2535, mRNA.

ACCESSION BE245100

VERSION BE245100.1 GI:9096842

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 549)

AUTHORS Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D.

, Bouck,J., Gibbs,R.A. and Margolin,J.F.

Pediatric Leukemia cDNA Sequencing Project

Unpublished (2000)

CONTACT: Dr. Judith F. Margolin

Texas Children's Cancer Center and Human Genome Sequencing Center

at Baylor College of Medicine

1102 Bates, MC3-3320 Houston, TX 77030, USA

Tel: 832-824-4536

seq documentation block:

17 sAsnGlyAsnMetMetAspTrpSerAsnPheSerThrGlnHisPheA 34
 57 GGATGGACCTTCGACCCCTGGTGGAGAACTCGTCGGTGGAGCGGTCA 106
 34 rGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50
 107 AGCAGCAGACGGAGTGCATGGTGCAGCAATACAGCAACTACAGC..... 150
 51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsnI 67
 151 ..GTAACGGGAGCGCGGTGACAGCTCGACACACCCCTCGGGGAGAACAT 197
 67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
 198 TGCGGACACGGGGGACTCAAGCGGCGCTACCGGGGTACCAAGACTGGG 247
 84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
 248 TAAAGAAGAACGGAGCTGACAGACGCTGCCACCCCTGGGTCTCACCAGC 297
 101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGlyCysLys 116
 298 AACGAGCTCTTCTCTAGGATTGCACAGTGTGGTCTGTCCGC 345

seq_name: gb_est2:BI869244

seq_documentation_block: 968 bp mRNA linear EST 11-Oct-2001
 LOCUS BI869244 603396112F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5406003.5
 DEFINITION mRNA sequence.

ACCESSION BI869244

VERSION BI869244.1 GI:16042917

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgc.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM12035 row: h column: 04

High quality sequence stop: 839.

Location/Qualifiers

FEATURES

source

1..968

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5406003"

/tissue_type="adenoecarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: liver; Vector: pCMV-SPORT6; Site:1: NotI;

Site:2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.7 Kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."

BASE COUNT 214 a 308 c 277 g 168 t

ORIGIN

alignment_scores:

Quality: 367.50

Ratio: 3.750

Length: 116

Gaps: 1

Percent Similarity: 84.483 Percent Identity: 53.448

alignment_block:

US-09-647-780A-4 x BI869244

Align seg 1/1 to: BI869244 from: 1 to: 968

1 GYHisGluIleThrHisGlyPheAspAsnGlyArgAsnPheAspLys 17
 192 GGCCATGAGCTGACTCATGCTTTTGTATGATCAAGGACGGAGTATGACAA 241
 17 sAsnGlyAsnMetMetAspTrpTrpSerAsnPheSerThrGlnHisPheA 34
 242 GGACGGGAACCTCCGGCCATGGTGAAGAACTCATCGTGGAGCCCTTCA 291
 34 rGluGlnSerGluCysMetIleTyrGlnTyrGlyAsnTyrSerTrpAsp 50
 292 AGCGTCAGACCGGAGTGTGATGAGCAGTACACCACTACAGC..... 335
 51 LeuAlaAspGluGlnAsnValAsnGlyPheAsnThrLeuGlyGluAsnI 67
 336 ..GTGAACGGGGAGCGGTGAACGGGGGGGACACACCTGGGGGAGAACAT 382
 67 eAlaAspAsnGlyGlyValArgGlnAlaTyrLysAlaTyrLeuLysTrpM 84
 383 CGCGCACACGGGGGTCTCAAGCGCGGCTATCGGGCTTACCAGAACTGGG 432
 84 eAlaGluGlyGlyLysAspGlnGlnLeuProGlyLeuAspLeuThrHis 100
 433 TGAAGAAGAACGGGGGTGAGCAGCTCGCTCCCGCCCTGGGGCTCACCANT 482
 101 GluGlnLeuPhePheIleAsnTyrAlaGlnValTrpCysGlyCysLys 116
 483 AACGAGCTCTTCTCTCTGGGGCTTGCACAGGCTGTGGTCTCCGTCGCCG 530

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2002, 11:05:27 ; Search time 11.88 Seconds
(without alignments)
378.070 Million cell updates/sec

Title: US-09-647-780A-4
Perfect score: 665
Sequence: 1 GHEITHGFDNCRNFDKNGN.....DLTHEQLFFINIAQWCGCK 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	469	70.5	749	1 NEP_HUMAN	P08473 homo sapien
2	469	70.5	749	1 NEP_RABIT	P08049 cryotolagus
3	468	70.4	749	1 NEP_MOUSE	O61391 mus musculus
4	465	69.9	749	1 NEP_RAT	P07861 rattus norv
5	374.5	56.3	754	1 ECE1_BOVIN	P42891 bos taurus
6	370.5	55.7	754	1 ECE1_CAVPO	P97739 cavia porce
7	370.5	55.7	762	1 ECE1_RAT	P42893 rattus norv
8	367.5	55.3	770	1 ECE1_HUMAN	P42892 homo sapien
9	353	53.1	749	1 PEX_HUMAN	P78562 homo sapien
10	351	52.8	749	1 PEX_MOUSE	P70669 mus musculus
11	343.5	51.7	765	1 ECE2_HUMAN	O60344 homo sapien
12	339.5	51.1	787	1 ECE2_BOVIN	Q10711 bos taurus
13	263	39.5	769	1 YCVL_CABEL	Q22523 caenorhabdi
14	166.5	25.0	647	1 PPEO_LACHE	O52071 lactobacill
15	165	24.8	626	1 PPEO_LACLA	Q07744 lactococcus
16	165	24.8	626	1 PPEO_LACLC	Q09145 lactococcus
17	163.5	24.6	564	1 YSC6_STRGC	P42359 streptococc
18	113	17.0	732	1 KELL_HUMAN	P23276 homo sapien
19	78	11.7	543	1 PROA_LEGPN	P21347 legionella
20	75.5	11.4	256	1 YREC_SYNP2	P19737 synechococc
21	74	11.1	529	1 PROA_LEGLO	P55110 legionella
22	73.5	11.1	1078	1 GYRB_SYNP3	P77966 synechocyst
23	71.5	10.8	328	1 Y915_STRPY	Q9A064 streptococc
24	70	10.5	999	1 RLK5_ARATH	P47735 arabidopsis
25	68.5	10.3	730	1 GLGB_HAEIN	P45177 haemophilus
26	68	10.2	565	1 HEMA_TAHUR	P17002 influenza a
27	68	10.2	647	1 CMF_ECOLI	P33927 escherichia
28	68	10.2	731	1 BAF1_YEAST	P14164 saccharomyc
29	67	10.1	362	1 COTH_BACSU	Q45535 bacillus su
30	67	10.1	608	1 VATI_BORBU	O51118 borrelia bu
31	66.5	10.0	328	1 Y095_STRPN	Q97160 streptococc
32	66.5	10.0	526	1 CLOS_CLOHI	P09870 clostridium
33	66.5	10.0	648	1 CMF_HAEIN	P45037 haemophilus

34	66	9.9	632	1 PARE_HAEIN	P43703 haemophilus
35	66	9.9	898	1 IF38_CABEL	O02328 caenorhabdi
36	65.5	9.8	224	1 MTGA_ACICA	O24849 acinetobact
37	65.5	9.8	847	1 HEX_VIBVU	O04786 vibrio vuln
38	65	9.8	265	1 SR21_SARPE	P24491 sarcophaga
39	65	9.8	500	1 ABFA_BACSU	P94531 bacillus su
40	65	9.8	942	1 HEX_ADEG1	P42671 avian adeno
41	64.5	9.7	627	1 TSD2_ABIGR	O24474 abies grand
42	64.5	9.7	1157	1 XNA_THESA	P36917 thermoanaer
43	64.5	9.7	1241	1 TRK1_SACBA	P28569 saccharomyc
44	64.5	9.7	2813	1 VWF_CANFA	Q28295 canis famil
45	64	9.6	631	1 THIC_SALTY	Q01917 salmonella

ALIGNMENTS

RESULT 1

ID	NEP_HUMAN	STANDARD	PRT	749 AA
AC	P08473			
DT	01-AUG-1988	(Rel. 08, Created)		
DT	01-AUG-1988	(Rel. 08, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Neprilysin (EC 3.4.24.11) (Neutral endopeptidase) (NEP)			
DE	(Enkephalinase) (Common acute lymphocytic leukemia antigen) (CALLA)			
DE	(Neutral endopeptidase 24.11) (CD10)			
GN	MME OR EPN			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo			
OX	NCBI_TaxID=9606			
RN	[1]			
RP	SEQUENCE OF 2-749 FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=8815222; PubMed=3162217;			
RA	Malfoy B., Kuang W.-J., Seeburg P.H., Mason A.J., Schofield P.R.;			
RT	"Molecular cloning and amino acid sequence of human enkephalinase (neutral endopeptidase)."			
RL	FEBS Lett. 229:206-210(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=89010526; PubMed=2971756;			
RA	Letarte M., Vera S., Tran R., Addis J.B.L., Onizuka R.J.,			
RT	Quackenbush E.J., Jongeneel C.V., McInnes R.R.;			
RL	"Common acute lymphocytic leukemia antigen is identical to neutral endopeptidase."			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=88263038; PubMed=2968607;			
RA	Shipp M.A., Richardson N.E., Sayre P.H., Brown N.R., Masteller E.L.,			
RT	Clayton L.K., Ritz J., Reinherz E.L.;			
RL	"Molecular cloning of the common acute lymphoblastic leukemia antigen (CALLA) identifies a type II integral membrane protein."			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=89386688; PubMed=2528730;			
RA	D'Adamo L., Shipp M.A., Masteller E.L., Reinherz E.L.;			
RT	"Organization of the gene encoding common acute lymphoblastic leukemia antigen (neutral endopeptidase 24.11): multiple minlexons and separate 5' untranslated regions."			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=94222095; PubMed=8168535;			
RA	Le Moual H., Dion N., Roques B.P., Crine P., Boileau G.;			
RT	"Asp650 is crucial for catalytic activity of neutral endopeptidase 24-11."			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=94222095; PubMed=8168535;			
RA	Le Moual H., Dion N., Roques B.P., Crine P., Boileau G.;			
RT	"Asp650 is crucial for catalytic activity of neutral endopeptidase 24-11."			
RN	[6]			

OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
OX	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=BALE/C.
RC	MEDLINE=92242908; PubMed=1374101;
RX	Chen C.Y., Salles G., Seldin M.F., Kister A.E., Reinher E.L.,
RA	Shipp M.A.;
RA	"Murine common acute lymphoblastic leukemia antigen (CD10 neutral
RT	endopeptidase 24.11). Molecular characterization, chromosomal
RT	localization, and modeling of the active site.";
RT	J. Immunol. 148:2817-2825(1992).
RL	
CC	-!- FUNCTION: THYMOLYSIN-LIKE SPECIFICITY, BUT IS ALMOST CONFINED ON
CC	ACTING ON POLYPEPTIDES OF UP TO 30 AMINO ACIDS. BIOLOGICALLY

CC		AND LEU-ENKEPHALINS BY CLEAVAGE OF A GLY-PHE BOND.
CC	-!	COPACITOR; BINDS I ZINC ION.
CC	-!	SUBCELLULAR LOCATION: Type II membrane protein.
CC	-!	SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE NEPRILYSIN SUBFAMILY.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licensed@isb-sib.ch)
CC		-----
CC	EMBL;	M81591; AAA37386.1; .
DR	HSSP;	P08473; IDMT.
DR	MEROPS;	M13.001; .
DR	MGD;	MGI:97004; Mne.
DR	InterPro;	IPR000718; Peptidase_M13.
DR	InterPro;	IPR000130; Zn_MTpeptdse.
DR	Pfam;	PF01431; Peptidase_M13; 1.
DR	PRINTS;	PR00786; NEPRILYSIN.
DR	PROSITE;	PS00142; ZINC_PROTEASE; 1.
KW	Hydrolyase; Metalloprotease; Zinc; Transmembrane; Glycoprotein;	
KW	Signal-anchor.	
FT	INIT MET	0
FT	DOMAIN	1..27
FT	TRANSMEM	28..50
FT		BY SIMILARITY
FT		CYTOPLASMIC (POTENTIAL)..
FT		SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	DOMAIN	51..749
FT		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	15..22
FT		STOP-TRANSFER SQUENCE (POTENTIAL).

[illegible]

FT	METAL	646	ZINC (CATALYTIC)	(BY SIMILARITY)
FT	ACT_SITE	650	PROTON DONOR (BY SIMILARITY)	
FT	CARBOHYD	144	N-LINKED (GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	210	N-LINKED (GLCNAC. .)	(POTENTIAL)

FT	CARBOHYD	284	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	310	N-LINKED (GLCNAC. . .) (BY SIMILARITY)

FT	CARBOHYD	324	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	627	N-LINKED (GLCNAC. . .) (BY SIMILIARITY)

	Query Match	--70.4%; Score 468; DB 1;	Length 749;	
	Best Local Similarity	65.8%;	Pred. NO. 9.2e-40;	
	Matches 75; Conservative 25;	Mismatches 14;	Indels 0;	Gaps 0;
OY	1	GHEITHGFDNDGRFNKDNMMDDWNSFTQHFRQSECHYYOYGNYSWDLADQNNGVF	60	
		: :		
		: :		
DB	582	GHEITHGFDDNDRNFNKDGLDVWDTHQQSANNEKDQSQCVMVYOYGNFSWDLAGLNGI	641	
		: :		
		: :		
	61.	NITIGENTADGGCBARAYIKWMAREGGDKDOOLPGFIDLTFOELFFNTYBQVWCFC	114	

```

FT ACT_SITE 650 PROTON DONOR (BY SIMILARITY).
FT CARBOHYD 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 210 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 284 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 310 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 324 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 627 N-LINKED (GLCNAC. .) (BY SIMILARITY).
SQ SEQUENCE 749 AA; 85663 MW; 89B0EC50A9016A47 CRC64;

Query Match 69.9%; Score 465; DB 1; Length 749;
Best Local Similarity 64.9%; Pred. No. 1.9e-39;
Matches 74; Conservative 26; Mismatches 14; Indels 0; Gaps

Qy 1 GHEITHGDDNGRNFDRKNGMMDWNSFSTQHFRQSECMYQYGNYSWDLADEQNVNGF 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 582 GHEITHGDDNGRNFENKDGDLVDWWTQSQANFNKFSQCMVYQYGNFTWDLAGGQHLNGI 641

Qy 61 NTLGENTADNGGVQAYKAYLKWMAEGGKDDQLPLGLDLTHEQLFFNYAQVWCG 114
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 642 NTLGENTADNGGIGQAYRAYQNTYVKNKEGKLLPLGLDLNKHQLFFLNFQAQVWCG 695

RESULT 5
ECEL_BOVIN STANDARD; PRT; 754 AA.
ID ECEL_BOVIN STANDARD; PRT; 754 AA.
AC P42891;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1).
GN ECE1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=9510423; PubMed=7805846;
RA Schmidt M., Kroeger B., Jacob E., Seulberger H., Subkowski T.,
RA Oter R., Meyer T., Schmalzing G., Hillen H.;
RT "Molecular characterization of human and bovine endothelin converting
RT enzyme (ECE-1).";
RL FEBS Lett. 356:238-243(1994).
CC -1- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1.
CC -1- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
CC Trp-1-Val-22 bond in the precursor.
CC -1- ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13 (ZINC
CC METALLOPROTEASE); ALSO KNOWN AS THE NEPRILYSIN SUBFAMILY.
CC

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entities requires a license agreement (See http://www.isb-sib.ch/anno-
or send an email to license@isb-sib.ch).

CC EMBL; 235306; CAA84547.1;
CC HSSP; P08473; 1DMT.
CC MEROPS; M13.002;
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; zn_M13ptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
KW Signal-anchor.
FT DOMAIN 1 52 CYTOPLASMIC (POTENTIAL).

```

FT	TRANSMEM	53	73	FT
FT	DOMAIN	74	754	FT
FT	METAL	591	591	FT
FT	ACT_SITE	592	592	FT
FT	METAL	595	595	FT
FT	METAL	651	651	FT
FT	ACT_SITE	655	655	FT
FT	CARBOHYD	150	150	FT
FT	CARBOHYD	171	171	FT
FT	CARBOHYD	194	194	FT
FT	CARBOHYD	254	254	FT
FT	CARBOHYD	300	300	FT
FT	CARBOHYD	345	345	FT
FT	CARBOHYD	367	367	FT
FT	CARBOHYD	523	523	FT
FT	CARBOHYD	616	616	FT
FT	CARBOHYD	635	635	FT
SQ	SEQUENCE	754 AA:	85616 MW: E9276GCCB8E6FF4C CRC64:	SQ

Query Match	56.3%;	Score 374.5;	DB 1;	Length 754;
Best Local Similarity	54.3%;	Pred. NO. 2.6e-30;		
Matches 63;	Conservative 23;	Mismatches 27;	Indels 3;	Gaps 1;

[illegible]

RESULT 6
ECBL_CAVPO
ID ECBL_CAVPO STANDARD; PRT; 754 AA.
AC P97739;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1).
GN ECBL
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
OC NCBI_TaxID=10141;
RN [1]
RX MEDLINE=96192242; PubMed=8624482;
RA Shima H., Yamanouchi M., Omori K., Sugiura M., Kawashima K.,
RA Sato T.;
RT "Endothelin-1 production and endothelin converting enzyme expression
RT by guinea pig airway epithelial cells.";
RL Biochem. Mol. Biol. Int. 37:1001-1010(1995).
CC -!- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1.
CC -!- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
CC Trp-1-Val-22 bond in the precursor.
CC -!- ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13 (ZINC
CC METALLOPROTEASE); ALSO KNOWN AS THE NEPRILYSIN SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S82653; AAB46734.1; .

DR	HSP; P08473; 1DMT.
DR	MEROPS; M13_002; -.
DR	InterPro; IPR000718; peptidase_M13.
DR	InterPro; IPR000130; Zn_Wtpeptdse.
DR	Pfam; PF01431; Peptide_M13; 1.
DR	PRINTS; PR00786; NEPRILYSIN.
DR	PROSITE; PS00142; ZINC_PROTEASE; 1.
KW	Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
KW	Signal-anchor.
FT	DOMAIN 1 52 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 53 73 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	DOMAIN 74 754 EXTRACELLULAR (POTENTIAL).
FT	METAL 591 591 ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT_SITE 592 592 BY SIMILARITY.
FT	METAL 595 595 ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL 651 651 ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT_SITE 655 655 PROTON DONOR (BY SIMILARITY).
FT	CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 254 254 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 346 346 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 367 367 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 523 523 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 635 635 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE 754 AA; 85772 MW; F0646C57FF2B8A0 CRC64;

Query Match 55.7%; Score 370.5; DB 1; Length 754;
Best Local Similarity 53.4%; Pred. No. 6.6e-30;
Matches 62; Conservative 23; Mismatches 28; Indels 3

Qy	1	GHEITHGFDNCRNFDPKNGNDWNSFSTQHFPRESECMYIOYGNYSMDLADQNWNFG	60
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	590	GHEUTHAFDDGREYDKDGLRPWWNSSVEAFPQQOTCEMVEOYNNYS---VNGPEPVNR	646
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Qy	61	NTLGENTADRGGVRQAYKAYKLWMAEGKDDQLPGLDLTHEQLFFNYAQVMCGCK	116
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	647	HTLGENTADNGGLKAARYATGVNVKNKGABEETPLTGLTNNOFLFGLGAQMCSVR	702
		: : : : : : : : : : : : : : : : : : : : : : : : :	

RESULT	7			
ECEL	RAT			
ID	ECEL	STANDARD;	PRT;	762 AA.
AC	P42893;	Q9WUY8;		
DT	01-NOV-1995	(Rel. 32, Created)		
DT	01-OCT-1996	(Rel. 34, Last sequence update)		
DT	01-MAR-2002	(Rel. 41, Last annotation update)		
DE	Endothelin-converting enzyme 1	(EC 3.4.24.71) (ECE-1).		
GN	ECEL			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM C).			
RC	TISSUE=Endothelial cells;			
RX	MEDLINE=94308046; PubMed=8034569;			
RA	Shimada K., Takahashi M., Tanzawa K.;			
RT	"Cloning and functional expression of endothelin-converting enzyme			
RL	from rat endothelial cells.";			
RT	J. Biol. Chem. 269:18275-18278(1994).			
RN	[2]			
RP	SEQUENCE OF 1-116 FROM N.A., ALTERNATIVE SPLICING, SUBCELLULAR			
RP	LOCATION, AND TISSUE SPECIFICITY.			
RC	TISSUE=Smooth muscle;			
RX	MEDLINE=99421637; PubMed=10491078;			
RA	Valdenaire O., Lepailleur-Enouf D., Egidy G., Thouard A., Barret A.,			
RA	Vanckx R., Tougaard C., Michel J.-B.;			
RT	"A fourth isoform of endothelin-converting enzyme (ECE-1) is generated			

DR	EMBL:	X91936;	CAG3015.1;	JOINED.
DR	EMBL:	X91937;	CAG3015.1;	JOINED.
DR	EMBL:	X91938;	CAG3015.1;	JOINED.
DR	EMBL:	X91939;	CAG3015.1;	JOINED.
DR	EMBL:	X91939;	CAG3015.1;	JOINED.
DR	EMBL:	X91924;	CAG3016.1;	JOINED.
DR	EMBL:	X91925;	CAG3016.1;	JOINED.
DR	EMBL:	X91926;	CAG3016.1;	JOINED.
DR	EMBL:	X91927;	CAG3016.1;	JOINED.
DR	EMBL:	X91928;	CAG3016.1;	JOINED.
DR	EMBL:	X91929;	CAG3016.1;	JOINED.
DR	EMBL:	X91930;	CAG3016.1;	JOINED.
DR	EMBL:	X91931;	CAG3016.1;	JOINED.
DR	EMBL:	X91932;	CAG3016.1;	JOINED.
DR	EMBL:	X91933;	CAG3016.1;	JOINED.
DR	EMBL:	X91934;	CAG3016.1;	JOINED.
DR	EMBL:	X91935;	CAG3016.1;	JOINED.
DR	EMBL:	X91936;	CAG3016.1;	JOINED.
DR	EMBL:	X91937;	CAG3016.1;	JOINED.
DR	EMBL:	X91938;	CAG3016.1;	JOINED.
DR	EMBL:	X91939;	CAG3016.1;	JOINED.
DR	EMBL:	D43698;	BAA07800.1;	-
DR	EMBL:	AB031742;	BAA83687.1;	-
DR	EMBL:	AL031005;	CAB19767.1;	-
DR	EMBL:	AJ130828;	CAB46443.1;	-
DR	EMBL:	X98272;	CAG66922.1;	-
DR	EMBL:	AL031728;	CAB52285.1;	-
DR	EMBL:	AF018034;	AAD21221.1;	-
DR	HSSP:	P08473;	LDMT.	-
DR	MEROPS:	M13.002;	-	-
DR	MIM:	600423;	-	-
DR	InterPro:	IPR000718;	Peptidase_M13.	-
DR	InterPro:	IPR000130;	Zn_MTpeptdse.	-
DR	Pfam:	PF01431;	Peptidase_M13; 1.	-
DR	PRINTS:	PR00786;	NEPRILYSIN.	-
DR	PROSITE:	PS00142;	ZINC_PROTEASE; 1.	-
KW	Hydrolase;	Metalloprotease;	Zinc;	Glycoprotein; Transmembrane;
KW	Hydrolase;	Metalloprotease;	Zinc;	Polymorphism.
KW	Signal-anchor;	Alternative splicing;	CYTOSOLASMIC (POTENTIAL).	-
FT	DOMAIN	1	68	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	TRANSMEM	59	89	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	90	770	ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	607	607	BY SIMILARITY.
FT	ACT_SITE	608	608	ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	611	611	ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	667	667	PHOTON DONOR (BY SIMILARITY).
FT	ACT_SITE	671	671	N-LINKED (GLCNAC..)
FT	CARBOHYD	166	166	N-LINKED (GLCNAC..)
FT	CARBOHYD	187	187	N-LINKED (GLCNAC..)
FT	CARBOHYD	210	210	N-LINKED (GLCNAC..)
FT	CARBOHYD	270	270	N-LINKED (GLCNAC..)
FT	CARBOHYD	316	316	N-LINKED (GLCNAC..)
FT	CARBOHYD	362	362	N-LINKED (GLCNAC..)
FT	CARBOHYD	383	383	N-LINKED (GLCNAC..)
FT	CARBOHYD	539	539	N-LINKED (GLCNAC..)
FT	CARBOHYD	632	632	N-LINKED (GLCNAC..)
FT	CARBOHYD	651	651	N-LINKED (GLCNAC..)
FT	VARSPLIC	1	44	MRGVPPVVSALLSALGMSYTKRAILEDLVDLSSEGDA
FT	FT	FT	FT	PNG -> MPQLGLQORNPFLOGKRGPGLTSTSPPLLP
FT	FT	FT	FT	(IN ISOFORM A).
FT	FT	FT	FT	MRGVPPVVSALLSALG -> MEALRESVLHLAQ (IN
FT	FT	FT	FT	ISOFORM D).
FT	FT	FT	FT	MRGVPPVVSALLSALG -> M (IN ISOFORM C).
FT	FT	FT	FT	T -> I (IN DBSNP:1076669).
FT	FT	FT	FT	/FTIG-VAR_011972.
FT	SEQUENCE	770 AA;	87163 MW;	DD88A59748B2F80 CRC64;

Query Match 55.3%; Score 367.5; DB 1; Length 770;
 Best Local Similarity 53.4%; Pred.No.1.4e-29;
 Matches 62; Conservative 21; Mismatches 30; Indels 3; Gaps
 OV 1 GHEITGFDNDGNRPDKNNMMDWNFSNFTSHFRFDSCEGMIVGYGNVSDIADFNVNCF 60

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE NEPRILYSIN SUBFAMILY.

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EMBL; AB011176; BAA25530.1; -
EMBL; AFJ92531; AAC28399.1; -
HSPG; P08473; IDMT.
MEROPS; M13.006; -.
InterPro; IPR000718; Peptidase_M13.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase.M13; 1.
PRINTS; PR00786; NEPRILYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolyase; Metalloprotease; Zinc; Glycoprotein; Transmembrane; Signal-anchor.
DOMAIN      1    60
TRANSMEM   61    81
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
ACT_SITE   602   602
METAL       603   603
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
METAL     606   606
ZINC (CATALYTIC) (BY SIMILARITY).
METAL     662   662
PROTON DONOR (BY SIMILARITY).
ACT_SITE   666   666
N-LINKED (GLCNAC...) (POTENTIAL).
CARBOHYD   161   161
N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 165   165
N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 206   206
N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 266   266
N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 311   311
N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 378   378
N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 534   534
N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 627   627
N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 635   635
N-LINKED (GLCNAC...) (POTENTIAL).
SEQUENCE   765 AA; 86469 MW; 89DLI8831B5628694 CRC64;
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Query Match
Best Local Similarity 51.7%; Score 343.5; DB 1; Length 765;
Matches 59; Conservative 18; Mismatches 36; Indels 3; Gaps 1;

Qy 1 CHEITHGEDDNRFDKNGNMWDWSNFSTOHFRSEQSCMYIQYGNVSNDLADQNVGTF 60
 | | | : | | | | | | | : | | | | | : | | | : | |
Db 601 CHETLFADFDDGREYDEKGNLRPWQNESLAAFRHNHTACMEEQNYQ---VNGELNRGR 657

Qy 61 NTLGENTADNGGVROAYKAYLKWAEGSKDOOLPCGLDLTHEQLFEINYAOWYCCK 116
 ||||| | | | | | | | | | | | | | | | | | | | | | | |
Db 658 QTLGENTADNGGLKAANYRAYRAWLKRHGEEQQLPAGVLTNHOLFVFVGAQCWCSVR 713

RESULT 12
ECE2_BOVIN STANDARD; PRT; 787 AA.
ID_ECE2_BOVIN
AC Q10711:
DT DT 01-OCT-1996 (Rel. 34, Created)
DT DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT DT 01-OCT-1996 (Rel. 34, Last annotation update)
DB Endothelin-converting enzyme 2 (EC 3.4.24.71) (ECC-2).
GN ECC2.
OS Bos taurus [Bovine].
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95318093; PubMed=7797512;

RA Emoto N., Yanagisawa M.;
RT "Endothelin-converting enzyme-2 is a membrane-bound, phosphoramidon-
RT sensitive metalloprotease with acidic pH optimum.";
RL J. Biol. Chem. 270:15262-15268 (1995).
CC -!- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1. OPTIMUM PH IS
CC 5.5. INACTIVE AT NEUTRAL PH.
CC -!- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
CC tripeptide bond in the precursor.
CC -!- ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13 (ZINC
CC METALLOPROTEASE); ALSO KNOWN AS THE NEPRILYSIN SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U27341; AAA82927.1;
DR HSSP; P08473; IDMT.
DR MEMOPS; M13.003;
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; Zn_MTPeptidse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
KW Signal-anchor.
FT DOMAIN 1 82
FT TRANSMEM 83 103
FT
FT DOMAIN 787
FT METAL 624
FT ACT_SITE 625
FT METAL 628
FT ACT_SITE 688
FT CARBOHYD 164
FT CARBOHYD 183
FT CARBOHYD 187
FT CARBOHYD 228
FT CARBOHYD 288
FT CARBOHYD 333
FT CARBOHYD 400
FT CARBOHYD 556
FT CARBOHYD 649
FT CARBOHYD 657
FT SEQUENCE 787 AA; 88957 MW; F085C2921DAF0BF2 CRC64;
Query Match 51.1%; Score 339.5; DB 1; Length 787;
Best Local Similarity 50.0%; Pred. No. 9.4e-27; Mismatches 36; Indels 3; Gaps 1;
Matches 58; Conservative 19;
QY 1 GHEITHGFDNGRNFDKNGNMDWNSFSTQHFRESECMYQYGNYSWDLADEQNVNGF 60
DB 623 GHEITHAFDDQGREYDKGNLRPWWQNESLAFNRHTACIEQYSQYQ---VNGEKLNGR 679
QY 61 NTLGENIADGGVQRYKAYLKWMAEGGKQDLPLGLDLTHEQLFFINAYQVWCCK 116
DB 680 QTLGENIADGGGLKAYNAYKAWLRKHGEQQLPAVGLTNHOLFVFGFAQVWCVR 735
RESULT 13
ID YCYL_CAEEL
AC Q22523;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical zinc metalloprotease T16A9.4 (EC 3.4.24.-).
GN T16A9.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA McMurray A.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS
RC STRAIN-BRISTOL N2;
RC Jones S.J.M.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13 (ZINC
CC METALLOPROTEASE); ALSO KNOWN AS THE NEPRILYSIN SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z71135; CAB00879.1;
DR HSSP; P08473; IDMT.
DR WormPep; T16A9.4; CE18259.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; Zn_MTPeptidse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hypothetical protein; Hydrolase; Metalloprotease; Zinc; Glycoprotein;
KW Transmembrane; Signal-anchor.
FT DOMAIN 1 26
FT TRANSMEM 27 47
FT
FT DOMAIN 48 769
FT METAL 601
FT ACT_SITE 602
FT METAL 605
FT METAL 663
FT ACT_SITE 667
FT CARBOHYD 69
FT CARBOHYD 221
FT CARBOHYD 240
FT CARBOHYD 272
FT CARBOHYD 307
FT CARBOHYD 356
FT CARBOHYD 412
FT CARBOHYD 506
FT CARBOHYD 684
FT CARBOHYD 698
FT SEQUENCE 769 AA; 88349 MW; EF6552CE49AA3928 CRC64;
Query Match 39.5%; Score 263; DB 1; Length 769;
Best Local Similarity 44.0%; Pred. No. 4.9e-19;
Matches 51; Conservative 21; Mismatches 40; Indels 4; Gaps 3;
QY 1 GHEITHGFDNGRNFDKNGNMDWNSFSTQHFRESECMYQYGNYSWDLADEQNVNGF 60
DB 600 GHEVSHAFDDQGGQYDEMGNDLNDWMDAETEEKEFIEKTRCFVQYVNVVYEA- IHLNGQ 658
QY 61 NTLGENIADGGVQRYKAYLKWMAE--GGKQDLPLGL-DLTHEQLFFINAYQVWC 113
DB 659 LSLGENIADGGVKTAFNAYKAWKSNWTGISSEPALPGFQNTSQQFFFLAYANWC 714

Mon Oct 7 11:24:40 2002

Search completed: October 3, 2002, 11:06:08
Job time: 41 sec

us-09-647-780a-4.rsp

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 3, 2002; 11:05:27 ; Search time 12.99 seconds
(without alignments)
218.119 Million cell updates/sec.

Title: US-09-647-780A-4
Perfect score: 665
Sequence: 1 GHEITHGFDDNGRNFKN.....DLTHEQLFFINVAQWVCCK 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pap.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pap.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pap.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	374.5	56.3	189	3	US-08-646-273-14
2	374.5	56.3	708	3	US-08-646-273-23
3	374.5	56.3	754	3	US-08-646-273-30
4	370.5	55.7	758	1	US-08-289-112-2
5	367.5	55.3	703	3	US-08-646-273-25
6	367.5	55.3	753	3	US-08-646-273-36
7	339.5	51.1	787	1	US-08-574-763-2
8	336.5	50.6	567	3	US-08-646-273-19
9	318.5	47.9	775	4	US-05-305-640-2
10	73	11.0	758	1	US-08-258-188-2
11	73	11.0	758	1	US-08-526-813-2
12	73	11.0	758	5	PCT-US95-08554-2
13	70	10.5	999	2	US-08-473-553A-5
14	68	10.2	2710	2	US-08-568-459A-12
15	68	10.2	2710	2	US-08-487-826B-12
16	68	10.2	3060	2	US-08-487-826B-14
17	67	10.1	914	4	US-09-437-054A-8
18	65	9.8	500	3	US-08-926-842B-64
19	65	9.8	942	4	US-09-171-461-12
20	64.5	9.7	474	2	US-08-282-197C-58
21	64.5	9.7	2813	3	US-08-896-449A-2
22	64.5	9.7	2813	3	US-09-132-652-2
23	64	9.6	919	4	US-09-437-054A-17
24	63.5	9.5	2050	2	US-08-347-594A-2
25	63	9.5	214	3	US-08-960-507-21
26	63	9.5	478	4	US-08-740-223A-7
27	63	9.5	490	4	US-08-740-223A-12

28	63	9.5	495	4	US-08-740-223A-26
29	63	9.5	495	4	US-09-351-457-5
30	63	9.5	495	4	US-09-561-500-5
31	63	9.5	495	4	US-09-561-108-5
32	63	9.5	496	4	US-08-740-223A-22
33	63	9.5	497	1	US-08-373-579-4
34	63	9.5	497	2	US-08-418-595-4
35	63	9.5	497	2	US-08-665-926-4
36	63	9.5	497	2	US-08-348-492-4
37	63	9.5	497	4	US-09-162-437-4
38	63	9.5	497	4	US-08-740-223A-14
39	63	9.5	498	1	US-08-373-579-2
40	63	9.5	498	2	US-08-418-595-2
41	63	9.5	498	2	US-08-665-926-2
42	63	9.5	498	2	US-08-348-492-2
43	63	9.5	498	4	US-09-162-437-2
44	63	9.5	498	4	US-08-740-223A-2
45	63	9.5	498	4	US-09-351-457-2

ALIGNMENTS

RESULT 1
US-08-646-273-14
; Sequence 14, Application US/08646273
; Patent No. 6066502

GENERAL INFORMATION:
APPLICANT: Kroeger, Burkhard, Seulerberger, Harald, Meyer, Thomas, Schmidt, Heine
APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Hein
TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kell & Weinlauf
STREET: 1101 Connecticut Avenue
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM AT-compatible, 80486 processor
OPERATING SYSTEM: MS-DOS version 6.0
SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,273
FILING DATE: 16-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03706
FILING DATE: 11-NOV-1994
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-273-14

Query Match 56.3%; Score 374.5; DB 3; Length 189;
Best Local Similarity 54.3%; Pred. No. 5.4e-36;
Matches 63; Conservative 23; Mismatches 27; Indels 3; Gaps 1;

QY	1	GHEITHGFDDNGRNFKNMNDWNSFSTQHFREQSECMYQYGNYSWDLADQNNGF	60
DB	25	GHEITHGFDDNGRNFKNMNDWNSFSTQHFREQSECMYQYGNYSWDLADQNNGF	81
QY	61	NTLGENIADNGVRQAYKAYLKWNAEGKQDQLPGLDLTHEQLFFINVAQWVCCK	116
DB	82	HTLGENIADNGGLKAAAYRAYONWVKNGAEGTLLTGLTNNQLFLSFAQWVCVR	137

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; FILING DATE: 16-NOV-1994
;
; -CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/03706
; FILING DATE: 11-NOV-1994
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 754 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-646-273-30
;
;
; Query Match 56.3%; Score 374.5; DB 3; Length 754;
; Best Local Similarity 54.3%; Pred. No. 3.4e-35;
; Matches 63; Conservative 23; Mismatches 27; Indels 3; Gaps
;
; QY 1 GHEITHGFDNCRNFKKGNMMDWWSNFSSTOHFRQSECMYIQVNYSWDLADQNVNGF 60
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; DB 590 GHETHAFDDQREYDKGNLRPPWKNKSVEAFKQOTACMYEQYGNYS--VNGEPVNGR 646
;
; QY 61 NTLGENIADNGVROYAKYKILKMAEGCKDQOLPGLDLTHEOLFFINVAOVWCCK 116
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; DB 647 HTLGENIADNGGLKAAAYRAYQNVNKKNGAEOETPLTGLTNQLFLSFAQVWCVR 702
;
;
; RESULT 4
; US-08-289-112-2
; ; Sequence 2, Application US/08289112
; ; Patent No. 5688640
; ; GENERAL INFORMATION:
; ; APPLICANT: Yanagisawa, Masashi
; ; TITLE OF INVENTION: Endothelin Converting Enzyme-1: A
; ; TITLE OF INVENTION: Membrane-Bound Metalloprotease That Catalyzes The
; ; TITLE OF INVENTION: Proteolytic Activation of Big Endothelin-1
; ; NUMBER OF SEQUENCES: 5
; ; CORRESPONDENCE ADDRESS:
; ; ADDRESSEE: Arnold, White & Durkee
; ; STREET: P. O. Box 4433
; ; CITY: Houston
; ; STATE: TX
; ; COUNTRY: USA
; ; ZIP: 77210-4433
; ; COMPUTER READABLE FORM:
; ; MEDIUM TYPE: Floppy disk
; ; COMPUTER: IBM PC compatible
; ; OPERATING SYSTEM: PC-DOS/MS-DOS
; ; SOFTWARE: Patent In Release #1.0, Version #1.25
; ; CURRENT APPLICATION DATA:
; ; APPLICATION NUMBER: US/08/289,112
; ; FILING DATE: 10-APR-1994
; ; CLASSIFICATION: 435
; ; ATTORNEY/AGENT INFORMATION:
; ; NAME: Parker, David L.
; ; REGISTRATION NUMBER: 32,165
; ; REFERENCE/DOCKET NUMBER: UTSD:414/PAR
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 713-787-1400
; ; TELEFAX: 713-789-2679
; ; TELEX: 79-0924
; ; INFORMATION FOR SEQ ID NO: 2:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 758 amino acids
; ; TYPE: amino acid
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
; ;
; ; US-08-289-112-2
;
;
; Query Match 55.7%; Score 370.5; DB 1; Length 758;
; Best Local Similarity 53.4%; Pred. No. 1e-34;
; Matches 62; Conservative 23; Mismatches 28; Indels 3; Gaps

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Matches 22; Conservative 18; Mismatches 25; Indels 26; Gaps 4;

QY 10 DNGRNFCKNG-----NMMDWSNFSTQHFROSECMYQYGNYSWDLADEQNVNG 59
DB 181 EHKNYFENGYDARHAAFLSDLSLADFSRQHAYRAVAITQOH-----WD----- 227
QY 60 FNTLGE--NIADNGGVQYKAYKWKMAEGG 88
DB 228 -EKIGELAGITRNADRSQSGKAYINYLENGG 257

RESULT 11
US-08-526-813-2
Sequence 2, Application US/08526813
Patent No. 5756293
GENERAL INFORMATION:
APPLICANT: Hall, Robert H.
APPLICANT: Xu, Jian Guo
TITLE OF INVENTION: A New and Distinctive DNA Sequence of E.
TITLE OF INVENTION: coli 0157:H7 and its use for the Rapid, Sensitive and
TITLE OF INVENTION: Specific Detection of 0157:H7 and Other Enterohemorrhagic
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,813
FILING DATE: 14-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-206-1
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-526-813-2

Query Match 11.0%; Score 73; DB 1; Length 758;
Best Local Similarity 24.2%; Pred. No. 4.1;
Matches 22; Conservative 18; Mismatches 25; Indels 26; Gaps 4;

QY 10 DNGRNFCKNG-----NMMDWSNFSTQHFROSECMYQYGNYSWDLADEQNVNG 59
DB 181 EHKNYFENGYDARHAAFLSDLSLADFSRQHAYRAVAITQOH-----WD----- 227
QY 60 FNTLGE--NIADNGGVQYKAYKWKMAEGG 88
DB 228 -EKIGELAGITRNADRSQSGKAYINYLENGG 257

RESULT 12

PCT-US95-08554-2
Sequence 2, Application PC/TUS9508554
GENERAL INFORMATION:
APPLICANT: Hall, Robert H.
APPLICANT: Xu, Jian Guo
TITLE OF INVENTION: A NEW AND DISTINCTIVE DNA SEQUENCE OF E.
TITLE OF INVENTION: coli 0157:H7 AND ITS USE FOR THE RAPID, SENSITIVE AND
TITLE OF INVENTION: SPECIFIC DETECTION OF 0157:H7 AND OTHER ENTEROHEMORRHAGIC
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08554
FILING DATE: 14-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280206, DHHSE135940
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08554-2

Query Match 11.0%; Score 73; DB 5; Length 758;
Best Local Similarity 24.2%; Pred. No. 4.1;
Matches 22; Conservative 18; Mismatches 25; Indels 26; Gaps 4;

QY 10 DNGRNFCKNG-----NMMDWSNFSTQHFROSECMYQYGNYSWDLADEQNVNG 59
DB 181 EHKNYFENGYDARHAAFLSDLSLADFSRQHAYRAVAITQOH-----WD----- 227
QY 60 FNTLGE--NIADNGGVQYKAYKWKMAEGG 88
DB 228 -EKIGELAGITRNADRSQSGKAYINYLENGG 257

RESULT 13
US-08-473-553A-5
Sequence 5, Application US/08473553A
Patent No. 5859338
GENERAL INFORMATION:
APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-60886/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 999 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-473-553A-5

Query Match 10.5%; Score 70; DB 2: Length 999;
Best Local Similarity 24.5%; Pred. No. 13;
Matches 26; Conservative 15; Mismatches 35; Indels 30; Gaps 6;

Qy 25 WSNFSTQHFREQ--SECMIYQVGNYSWDLADEQNVNGFNTLGE--NIADNGGVROYAKAY 80
Db 666 WRSFKHLFSEHETADCL-----DEKNVIGFGSSGKVKYKVELRGGEVAVKK- 712

Qy 81 LKMAEGGKDOQLFDLTHQLFFI-----NYAQWCCG 115
Db 713 LNKSVKGGDDEV--SSDSLNRDVFAAEVETLGTIRHKSVLRWMC 756

RESULT 14
US-08-568-459A-12
Sequence 12, Application US/08568459A
Patent No. 5849306
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellem, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,459A
FILING DATE: 07-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
```

```
REFERENCE/DOCKET NUMBER: NIH121.001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
US-08-568-459A-12

Query Match 10.2%; Score 68; DB 2: Length 2710;
Best Local Similarity 21.5%; Pred. No. 85;
Matches 23; Conservative 21; Mismatches 35; Indels 28; Gaps 5;

Qy 2 HEITHGFDGNGNFKNG-----NMMDWNSFSTQHFREQSECMIYQY----- 44
Db 1483 NDVAKAKDKIGKFFSKDGSKSPSLRSQEWKTKNGPEIWKGL-CALTRYVTDNKRKI 1541

Qy 45 -GNYSWDLADEQNVNGFNTLGENIADNGGVROYAKAYLAKMAEGGKD 90
Db 1542 KNDYSYDKVN-OSQNGNPSLEEPAK-----POFLRWMIWEGEE 1579

RESULT 15
US-08-487-826B-12
Sequence 12, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellem, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
```

```

; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
US-08-487-826B-12

```

```

Query Match      10.2%; Score 68; DB 2; Length 2710;
Best Local Similarity 21.5%; Pred. No. 85;
Matches 23; Conservative 21; Mismatches 35; Indels 28; Gaps 5;

QY  2 HEITGFDNGRNFQKNG-----NMMDWSNFTQHFREQSECMIYQY----- 44
Db  1483 NDVAKAKDKIGFFSKDGSGLSPSQEWKTINGPEIWKGL-CALTRYVTDNKRKI 1541

QY  45 -GNYSWDLADEQNVNCFNTLGENIADNGGVRQAYKAYLKWMAEGGKD 90
Db  1542 KNDYSTYKVN-QSQNGNPSLEEFK-----POFLRMIEWGEE 1579

```

Search completed: October 3, 2002, 11:05:49
Job time: 22 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2002, 11:05:27 ; Search time 24.7 Seconds
(without alignments)

Title: US-09-647-780A-4
Perfect score: 665
Sequence: 1 GHEITHGFDDNGRNFDKNGN.....DLTHEQLFFINYAQVWCGCK 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: . . . 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters:

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*

- ```

1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_unclassified:*
14: sp_virus:*
15: sp_virus:*
16: sp_viruses:*
17: sp.archaea:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Query % |      | Score | Match  | Length  | DB | ID      | Description         |
|------------|---------|------|-------|--------|---------|----|---------|---------------------|
|            |         |      |       |        |         |    |         |                     |
| 1          | 651     | 97.9 | 4     | Q96PH9 | 770     | 4  | Q96PH9  | Q96ph9 homo sapien  |
| 2          | 581     | 87.4 | 742   | 11     | Q9ERK3  |    | Q9ERK3  | Q9erk3 mus musculu  |
| 3          | 581     | 87.4 | 742   | 11     | Q9JLI3  |    | Q9JLI3  | Q9jli3 mus musculu  |
| 4          | 581     | 87.4 | 779   | 11     | Q9ERK2  |    | Q9ERK2  | Q9erk2 mus musculu  |
| 5          | 577     | 86.8 | 742   | 11     | Q9QZV6  |    | Q9QZV6  | Q9qzv6 mus musculu  |
| 6          | 577     | 86.8 | 765   | 11     | Q9QZV7  |    | Q9QZV7  | Q9qzv7 mus musculu  |
| 7          | 434     | 65.3 | 770   | 13     | Q93394  |    | Q93394  | Q93394 perca flave  |
| 8          | 397.5   | 59.8 | 661   | 5      | Q9W435  |    | Q9W435  | Q9w435 drosophila   |
| 9          | 374.5   | 56.3 | 628   | 6      | Q28868  |    | Q28868  | Q28868 bos taurus   |
| 10         | 370.5   | 55.7 | 758   | 6      | Q28010  |    | Q28010  | Q28010 bos taurus   |
| 11         | 362.5   | 54.5 | 752   | 13     | Q9QGN6  |    | Q9QGN6  | Q9qgn6 gallus gall  |
| 12         | 351     | 52.8 | 749   | 11     | Q35812  |    | Q35812  | Q35812 rattus norv  |
| 13         | 348.5   | 52.4 | 750   | 5      | O44857  |    | O44857  | O44857 caenorhabdi  |
| 14         | 343.5   | 51.7 | 736   | 4      | Q96NX3  |    | Q96NX3  | Q96nx3 homo sapien  |
| 15         | 343.5   | 51.7 | 787   | 4      | Q96NXX4 |    | Q96NXX4 | Q96nxx4 homo sapien |
| 16         | 341.5   | 51.4 | 766   | 5      | Q18673  |    | Q18673  | Q18673 caenorhabdi  |

|    |       |      |      |    |                    |
|----|-------|------|------|----|--------------------|
| 17 | 338.5 | 50.9 | 763  | 5  | Q9XZ01-            |
| 18 | 338   | 50.8 | 848  | 5  | Q16796             |
| 19 | 336.5 | 50.6 | 763  | 11 | Q92366             |
| 20 | 323.5 | 48.6 | 193  | 5  | Q95SM2             |
| 21 | 323   | 48.6 | 726  | 5  | Q9W5Y0             |
| 22 | 321   | 48.3 | 772  | 5  | Q9BLH1             |
| 23 | 318.5 | 47.9 | 775  | 4  | Q9NY95             |
| 24 | 318.5 | 47.9 | 775  | 4  | Q95672             |
| 25 | 313.5 | 47.1 | 770  | 5  | Q9URP2             |
| 26 | 306.5 | 46.1 | 775  | 11 | Q9JHL3             |
| 27 | 306.5 | 46.1 | 775  | 11 | Q9JMT0             |
| 28 | 300.5 | 45.2 | 787  | 5  | Q9UA44             |
| 29 | 285   | 42.9 | 683  | 5  | Q9YL36             |
| 30 | 285   | 42.9 | 700  | 5  | Q9VAS0             |
| 31 | 274   | 41.2 | 717  | 5  | Q9AXY0             |
| 32 | 257   | 38.6 | 754  | 5  | Q19831             |
| 33 | 253   | 38.0 | 1589 | 2  | Q45569             |
| 34 | 240.5 | 36.2 | 689  | 2  | Q50642             |
| 35 | 239.5 | 36.0 | 507  | 5  | Q9GTU5             |
| 36 | 237   | 35.6 | 702  | 5  | Q9VH36             |
| 37 | 230.5 | 34.7 | 837  | 5  | Q76751             |
| 38 | 228.5 | 34.4 | 682  | 5  | Q3VAS2             |
| 39 | 223.5 | 33.6 | 700  | 16 | Q9PFT1             |
| 40 | 222.5 | 33.5 | 793  | 5  | Q25051             |
| 41 | 222.5 | 33.5 | 823  | 5  | Q45131             |
| 42 | 218.5 | 32.9 | 667  | 16 | Q06075             |
| 43 | 215.5 | 32.4 | 798  | 5  | Q22763             |
| 44 | 208   | 31.3 | 870  | 5  | Q9GTU6             |
| 45 | 205   | 30.8 | 787  | 5  | Q23684             |
|    |       |      |      |    | Q9XZ01 drosophila  |
|    |       |      |      |    | Q16796 caenorhabdi |
|    |       |      |      |    | Q92366 mus musculu |
|    |       |      |      |    | Q95SM2 drosophila  |
|    |       |      |      |    | Q9W5Y0 drosophila  |
|    |       |      |      |    | Q9BLH1 bombyx mori |
|    |       |      |      |    | Q9NY95 homo sapien |
|    |       |      |      |    | Q95672 homo sapien |
|    |       |      |      |    | Q9URP2 hydra atten |
|    |       |      |      |    | Q9JHL3 rattus norv |
|    |       |      |      |    | Q9JMT0 mus musculu |
|    |       |      |      |    | Q9UA44 aplysia cal |
|    |       |      |      |    | Q9YL36 drosophila  |
|    |       |      |      |    | Q9VAS0 drosophila  |
|    |       |      |      |    | Q9AXY0 drosophila  |
|    |       |      |      |    | Q19831 caenorhabdi |
|    |       |      |      |    | Q45569 caenorhabdi |
|    |       |      |      |    | Q50642 porphyromon |
|    |       |      |      |    | Q9GTU5 ancylostoma |
|    |       |      |      |    | Q9VH36 drosophila  |
|    |       |      |      |    | Q76751 haemonchus  |
|    |       |      |      |    | Q9VAS2 drosophila  |
|    |       |      |      |    | Q9PFT1 xyella fas  |
|    |       |      |      |    | Q25051 haemonchus  |
|    |       |      |      |    | Q45131 haemonchus  |
|    |       |      |      |    | Q06075 mycobacteri |
|    |       |      |      |    | Q22763 caenorhabdi |
|    |       |      |      |    | Q9GTJ6 ancylostoma |
|    |       |      |      |    | Q23684 caenorhabdi |

## ALIGNMENTS

|            |                                                       |
|------------|-------------------------------------------------------|
| RESULT     | 1                                                     |
| Q96PH9     |                                                       |
| ID         | PRELIMINARY; PRT; 770 AA.                             |
| AC         | Q96PH9;                                               |
| DT         | 01-DEC-2001 (Tremblrel 19, Created)                   |
| DD         | 01-DEC-2001 (Tremblrel 19, Last sequence update)      |
| DT         | 01-DEC-2001 (Tremblrel 19, Last annotation update)    |
| DE         | NPRILYSIN-LIKE METALLOPEPTIDASE 2.                    |
| OS         | Homo sapiens (Human).                                 |
| OC         | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;   |
| OX         | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea  |
| NCBI_TaxId | =9606.                                                |
| RN         | [1]                                                   |
| SEQUENCE   | FROM N.A.                                             |
| RP         | MEDLINE=21444797; PubMed=11560781;                    |
| RX         | Bonvouloir N., Lemieux N., Crine P., Boileau G., Des  |
| RT         | "Molecular cloning, tissue distribution, and chromoso |
| RR         | of WML2, a gene coding for a novel human member of    |
| RT         | endopeptidase-24.11 family.;"                         |
| RT         | DNA Cell Biol. 20:493-498(2001).                      |
| RL         | EMBL; AF36981; AAL08942.1 -                           |
| SQ         | SEQUENCE 770 AA; 88523 MW;                            |
| DR         | DF9C084AA56A21R CRC                                   |

```

Query Match - 97.9%; Score 651; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 4e-58;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Caps 0;

```

|    |     |                 |          |          |         |          |         |      |     |
|----|-----|-----------------|----------|----------|---------|----------|---------|------|-----|
| QY | 1   | GHEITHGFDDNGRNF | DKNGMMDW | SNFSTQHF | REQSECM | IYQYGNYS | WDLADQN | VNGF | 60  |
|    |     |                 |          |          |         |          |         |      |     |
| Db | 603 | GHEITHGFDDNGRNF | DKNGMMDW | SNFSTQHF | REQSECM | IYQYGNYS | WDLADQN | VNGF | 662 |

61 NTLGNIADNGVRQAYKAYLKWMAEGSKDQQLPGLDLTHEQLFFINYAQVWCG 114  
 QY  
 663 NTLGNIADNGVRQAYKAYLKWMAEGSKDQQLPGLDLTHEQLFFINYAQVWCG 716  
 Db

RESULT  
Q9ERK3

```
ID Q9ERK3 PRELIMINARY; PRT; 742 AA.
AC Q9ERK3; 2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE NEPRILYSIN-LIKE PEPTIDASE ALPHA.
GN MELL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1].
RP SEQUENCE FROM N.A.
RX MEDLINE=21293028; PubMed=11278416;
RA Shirotani K., Tsubuki S., Iwata N., Takaki Y., Harigaya W.,
RA Maruyama K., Kiyu-Seo S., Kiyama H., Iwata H., Tomita T.,
RA Iwatsubo T., Saido T.C.;
RT "Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42 Most
RT Rapidly and Efficiently among Thiorphan- and Phosphoramidon-sensitive
RT Endopeptidases."
RL J. Biol. Chem. 276:21895-21901(2001).
RL EMBL; AF302075; AAG18446.1;
DR HSSP; P08473; 1DMT.
DR MEROPS; M13.008;
DR MGD; MGI:1351603; Mell1.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; Zn_Mtpeptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN.1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN.1.
SQ SEQUENCE 742 AA; 85993 MW; 4A44EAD211B2499F CRC64;

Query Match 87.4%; Score 581; DB 11; Length 742;
Best Local Similarity 85.1%; Pred. No. 5.5e-51;
Matches 97; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEITHGDDNGRNFCKNGNMMDWSNFSTQHFREQSECMYQYGNYSWDLADEQNNGVF 60
DB 575 GHEITHGDDNGRNFCKNGNMMDWSNFSTQHFREQSECMYQYGNYSWDLADEQNNGVF 634
QY 61 NTLGENIADNGGVQRAYKAYLKWMAEGGKQDLPLGLDLTHEQLFFINYAQVWCG 114
DB 635 STLGENIADNGGVQRAYKAYLRLWLDGKQDLPLGLNLTYAQVWCG 688

RESULT 3
Q9JLI3 PRELIMINARY; PRT; 765 AA.
AC Q9JLI3; 2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE NEPRILYSIN-LIKE METALLOPEPTIDASE 1 (NEPRILYSIN-LIKE PEPTIDASE
DE BETA)
GN MELL1 OR SEP OR NL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1].
RP SEQUENCE FROM N.A.
RX TISSUE=TESTIS;
RX PubMed=10749671;
RA Ghaddar G., Ruchon A.F., Carpentier M., Marcinkiewicz M., Seidah N.G.,
RA Crine P., DesGroselliers L., Boileau G.;
RT "Molecular cloning and biochemical characterization of a new mouse
RT testis soluble zinc-metalloproteinase of the neprilysin family."
RL Biochem. J. 347:419-429(2000).
RN [2].
RP SEQUENCE FROM N.A.
RA Shirotani K., Saido T.C.;
RT "Cloning of neprilysin-like peptidase cDNAs."
```

```
Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF176569; AAF69247.1;
DR EMBL; AF302076; AAG18447.1;
DR HSSP; P08473; 1DMT.
DR MEROPS; M13.008;
DR MGD; MGI:1351603; Mell1.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; Prenyltn.
DR InterPro; IPR000130; Zn_Mtpeptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN.1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN.1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN.1.
SQ SEQUENCE 765 AA; 88699 MW; D3662F1CE5B957F7 CRC64;

Query Match 87.4%; Score 581; DB 11; Length 765;
Best Local Similarity 85.1%; Pred. No. 5.7e-51;
Matches 97; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEITHGDDNGRNFCKNGNMMDWSNFSTQHFREQSECMYQYGNYSWDLADEQNNGVF 60
DB 598 GHEITHGDDNGRNFCKNGNMMDWSNFSTQHFREQSECMYQYGNYSWDLADEQNNGVF 657
QY 61 NTLGENIADNGGVQRAYKAYLKWMAEGGKQDLPLGLDLTHEQLFFINYAQVWCG 114
DB 658 STLGENIADNGGVQRAYKAYLRLWLDGKQDLPLGLNLTYAQVWCG 711

RESULT 4
Q9ERK2 PRELIMINARY; PRT; 779 AA.
AC Q9ERK2; 2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE NEPRILYSIN-LIKE PEPTIDASE GAMMA.
GN MELL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1].
RP SEQUENCE FROM N.A.
RX MEDLINE=21293028; PubMed=11278416;
RA Shirotani K., Tsubuki S., Iwata N., Takaki Y., Harigaya W.,
RA Maruyama K., Kiyu-Seo S., Kiyama H., Iwata H., Tomita T.,
RA Iwatsubo T., Saido T.C.;
RT "Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42 Most
RT Rapidly and Efficiently among Thiorphan- and Phosphoramidon-sensitive
RT Endopeptidases."
RL J. Biol. Chem. 276:21895-21901(2001).
RL EMBL; AF302077; AAG18448.1;
DR HSSP; P08473; 1DMT.
DR MEROPS; M13.008;
DR MGD; MGI:1351603; Mell1.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; Zn_Mtpeptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN.1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN.1.
SQ SEQUENCE 779 AA; 89709 MW; 5E48CA530828584B CRC64;

Query Match 87.4%; Score 581; DB 11; Length 779;
Best Local Similarity 85.1%; Pred. No. 5.8e-51;
Matches 97; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEITHGDDNGRNFCKNGNMMDWSNFSTQHFREQSECMYQYGNYSWDLADEQNNGVF 60
DB 612 GHEITHGDDNGRNFCKNGNMMDWSNFSTQHFREQSECMYQYGNYSWDLADEQNNGVF 671
QY 61 NTLGENIADNGGVQRAYKAYLKWMAEGGKQDLPLGLDLTHEQLFFINYAQVWCG 114
```

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Db 672 STLGENIADNGGVRQAYKAYLRLWLDGGKQDRLPGLNLTVAQLFFINYAQVWCG 725
RESULT 5
Q9QZV6 PRELIMINARY; PRT; 742 AA.
AC Q9QZV6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SOLUBLE SECRETED ENDOPEPTIDASE DELTA.
GN MELL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20011457; PubMed=10542292;
RA Ikeda K., Emoto N., Raharjo S.B., Nurhantari Y., Saiki K.,
RA Yokoyama M., Matsuo M.;
RT "Molecular identification and characterization of novel membrane-bound
RT metalloprotease, the soluble secreted form of which hydrolyzes a
RT variety of vasoactive peptides."
RL J. Biol. Chem. 274:32469-32477(1999).
DR EMBL; AF157106; AAF13153.1;
DR HSSP; P08473; 1DWT.
DR MEROPS; M13.008;
DR MGD; MGI:1351603; Meil1.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; Zn_MTPeptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 742 AA; 85945 MW; CF5FF9D982471157 CRC64;

Query Match 86.8%; Score 577; DB 11; Length 742;
Best Local Similarity 84.2%; Pred. No. 1.4e-50;
Matches 96; Conservative 15; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEITHGFDNGRNFKNMGMDWNSFSTQHFREQSECMYQYGNYSWDLADQNNGVF 60
Db 575 GHEITHGFDNGRNFKNMGMDWNSFSAHFQQSQCMYQYGNFSWELADQNNGVF 634
QY 61 NTLGENIADNGGVRQAYKAYLKWAEKGKQDQLPGLDLTHEQLFFINYAQVWCG 114
Db 635 SSLGENIADNGGVRQAYKAYLRLWLDGGKQDRLPGLNLTVAQLFFINYAQVWCG 688

RESULT 6
Q9QZV7 PRELIMINARY; PRT; 765 AA.
AC Q9QZV7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SOLUBLE SECRETED ENDOPEPTIDASE.
GN MELL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20011457; PubMed=10542292;
RA Ikeda K., Emoto N., Raharjo S.B., Nurhantari Y., Saiki K.,
RA Yokoyama M., Matsuo M.;
RT "Molecular identification and characterization of novel membrane-bound
RT metalloprotease, the soluble secreted form of which hydrolyzes a
RT variety of vasoactive peptides."
RL J. Biol. Chem. 274:32469-32477(1999).

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DR EMBL; AF157105; AAF13152.1;
DR HSSP; P08473; 1DWT.
DR MEROPS; M13.008;
DR MGD; MGI:1351603; Meil1.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; Zn_MTPeptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 765 AA; 88651 MW; 567D3C17764C0F3F CRC64;

Query Match 86.8%; Score 577; DB 11; Length 765;
Best Local Similarity 84.2%; Pred. No. 1.5e-50;
Matches 96; Conservative 15; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEITHGFDNGRNFKNMGMDWNSFSTQHFREQSECMYQYGNYSWDLADQNNGVF 60
Db 598 GHEITHGFDNGRNFKNMGMDWNSFSAHFQQSQCMYQYGNFSWELADQNNGVF 657
QY 61 NTLGENIADNGGVRQAYKAYLKWAEKGKQDQLPGLDLTHEQLFFINYAQVWCG 114
Db 658 SSLGENIADNGGVRQAYKAYLRLWLDGGKQDRLPGLNLTVAQLFFINYAQVWCG 711

RESULT 7
Q93394 PRELIMINARY; PRT; 770 AA.
AC Q93394;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE NEPRILYSIN.
GN NEP1.
OS Perca flavescens (Yellow perch).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Percidae; Perca.
OX NCBI_TaxID=8167;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-OVULATORY OVARY.
RX MEDLINE=99445407; PubMed=10514552;
RA Langenau D.M., Goetz F.W., Roberts S.B.;
RT "The upregulation of messenger ribonucleic acids during 17alpha,
RT 20beta-dihydroxy-4-pregnen-3-one-induced ovulation in the perch
RT ovary."
RL J. Mol. Endocrinol. 23:137-152(1999).
DR EMBL; AF077612; AAC28366.1;
DR HSSP; P08473; 1DWT.
DR MEROPS; M13.001;
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; Zn_MTPeptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 770 AA; 88135 MW; D29F216CB041BACC CRC64;

Query Match 65.3%; Score 434; DB 13; Length 770;
Best Local Similarity 62.3%; Pred. No. 6.1e-36;
Matches 71; Conservative 25; Mismatches 18; Indels 0; Gaps 0;

QY 1 GHEITHGFDNGRNFKNMGMDWNSFSTQHFREQSECMYQYGNYSWDLADQNNGVF 60
Db 603 GHEITHGFDNGRNFKNMGMDWNSFSAHFQQSQCMYQYGNFSWELADQNNGVF 662
QY 61 NTLGENIADNGGVRQAYKAYLKWAEKGKQDQLPGLDLTHEQLFFINYAQVWCG 114
Db 663 NTLGENIADNGGVRQAYKAYLKWAEKGKQDQLPGLDLTHEQLFFINYAQVWCG 716

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RESULT 8
Q9W435 PRELIMINARY; PRT; 661 AA.
AC Q9W435;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CG5894 PROTEIN.
GN CG5894.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Folsler C., Gabrielian A.C., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003436; AAF46125.1;
DR HSSP; P08473; 1DWT.
DR MEOPS; M13 UPW;
DR FlyBase; FBgn0029843; Nepl.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; Zn_Mtpeptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 661 AA; 76226 MW; 76DD13FC3BC066A5 CRC64;
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Query Match 59.8%; Score 397.5; DB 5; Length 661;
Best Local Similarity 59.6%; Pred. No. 2.8e-32;
Matches 68; Conservative 21; Mismatches 24; Indels 1; Gaps 1;
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QY 1 GHEITHGFDNGRNFKNMMDWNFSTQHFRESECMYQYGNYSWDLADQNNGF 60
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Db 495 GHEITHGFDKGRQFDKNGNMWNNATIAFRRTQCVIDQYSRYKINEVD-NFMDGR 553
QY 61 NTLGENIADNGVRQAYKAYLKWMAEGGKDDQLPGLDLTHEQLFFINIAQVCG 114
Db 554 MTOGENIADNGGLKQAFRAYKKWETLHGREQQLPGLNMTHTDQLFFINIAQIWC 607
RESULT 9
Q28868 PRELIMINARY; PRT; 758 AA.
AC Q28868;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ENDOTHELIN CONVERTING ENZYME.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95032010; PubMed=7945289;
RA Ikura T., Sawamura T., Shiraki T., Hosokawa H., Kido T., Hoshikawa H.,
RA Shinada K., Tanzawa K., Kobayashi S., Miwa S., et al.;
RT "cDNA cloning and expression of bovine endothelin converting enzyme.";
RL Biochem. Biophys. Res. Commun. 203:1417-1422(1994).
DR EMBL; S73774; AAB32062.1;
DR HSSP; P08473; 1DWT.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; Zn_Mtpeptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 758 AA; 85648 MW; 6A7EA96566BEFEC5 CRC64;
Query Match 56.3%; Score 374.5; DB 6; Length 758;
Best Local Similarity 54.3%; Pred. No. 7.3e-30;
Matches 63; Conservative 23; Mismatches 27; Indels 3; Gaps 1;
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```
QY 1 GHEITHGFDNGRNFKNMMDWNFSTQHFRESECMYQYGNYSWDLADQNNGF 60
Db 594 GHEITHAFDDQGREYDKDGNLRPWKNSSVEAFKQQTACHVEQYGNYS---VNGEPVNGR 650
QY 61 NTLGENIADNGVRQAYKAYLKWMAEGGKDDQLPGLDLTHEQLFFINIAQVCGCK 116
Db 651 HTLGENIADNGGLKAAAYRAYQNVKNGAEQTLPTLGLTNQLFSLFAQVWCVSVR 706
```

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RESULT 10
Q28010 PRELIMINARY; PRT; 758 AA.
AC Q28010;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ENDOTHELIN CONVERTING ENZYME-1A.
GN ECE-1A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94340737; PubMed=8062389;
RA Xu D., Emoto N., Giald A., Slaughter C., Kaw S., deWit D.,
RA Yanagisawa M.,
RT "ECE-1: a membrane-bound metalloprotease that catalyzes the
RT proteolytic activation of big endothelin-1";
RL Cell 78:473-485(1994).
```



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RN [2]
RP SEQUENCE FROM N.A.
RA Yanagisawa M.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U27342; AAA82928.1; -
DR HSP; P08473; IDMT.
DR MEROPS; M13.002; -
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; Zn_MTPeptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 758 AA; 85620 MW; 39DCB702099F40A4 CRC64;

Query Match
Best Local Similarity 53.4%; Score 370.5; DB 6; Length 758;
Matches 62; Conservative 23; Mismatches 28; Indels 3; Gaps 1;

QY 1 GHEITHGFDNGRNFDRKNGNMWNSFSTQHFREQSECMYQYGNYSWDLADQNVNGF 60
Db 594 GHEITHAFDDQGREYDKDGNLRPWKNSVVEAFKQTACMVQYGNYS---VNGEPVNGR 650
QY 61 NTLGENTADNGVRQAYKAYLKWMAEGGKDQQLPGLDLTHEOLFNFYNAQVWCCK 116
Db 651 HTLGENIADNGGLKAARYAYQVWYKNGAEOTLTGLTNHQLFSLFGQVWCYSVR 706

RESULT 11
Q9DGN6
ID Q9DGN6 PRELIMINARY; PRT; 752 AA.
AC Q9DGN6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENDOTHELIN CONVERTING ENZYME-1.
GN ECE-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20363660; PubMed-10903177;
RX Takebayashi-Suzuki K., Yanagisawa M., Gourdie R.G., Kanzawa N.,
RA Mikawa T.;
RT "In vivo induction of cardiac Purkinje fiber differentiation by
RT coexpression of preproendothelin-1 and endothelin converting enzyme-
RT 1.";
RL Development 127:3523-3532(2000).
DR EMBL; AF230274; AAF98287.1; -
DR HSP; P08473; IDMT.
DR MEROPS; M13.002; -
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; Zn_MTPeptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 752 AA; 84985 MW; 3B6B3DB7BF900656 CRC64;

Query Match
Best Local Similarity 54.5%; Score 362.5; DB 13; Length 752;
Matches 60; Conservative 24; Mismatches 29; Indels 3; Gaps 1;

QY 1 GHEITHGFDNGRNFDRKNGNMWNSFSTQHFREQSECMYQYGNYSWDLADQNVNGF 60
Db 588 GHEITHAFDDQGREYDKDGNLRPWKNSVVEAFKQTACMVQYGNYS---VNGEPVNGR 650
QY 61 NTLGENTADNGVRQAYKAYLKWMAEGGKDQQLPGLDLTHEOLFNFYNAQVWCCK 116
Db 645 HTLGENIADNGGLKAARYAYQVWYKNGAEOTLTGLTNHQLFSLFGQVWCYSVR 700
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RESULT 12
Q35812
ID Q35812 PRELIMINARY; PRT; 749 AA.
AC Q35812;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PHEX PROTEIN.
GN PHEX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-97343325; PubMed=9199930;
RA Francis F., Strom T.M., Hennig S., Boeddrich A., Lorenz B.,
RA Brandau O., Mohrke K.L., Cagnoli M., Steffens C., Klages S.,
RA Borzym K., Pohl T., Oudet C., Econs M.J., Rowe P.S., Reinhardt R.,
RA Weisinger T., Lehrach H.;
RT "Genomic organization of the human PEX gene mutated in X-linked
RT dominant hypophosphatemic rickets.";
RL Genome Res. 7:573-585(1997).
DR EMBL; AJ001637; CAA04890.1; -
DR HSP; P08473; IDMT.
DR MEROPS; M13.091; -
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; Zn_MTPeptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 749 AA; 86305 MW; 690B8E2609C1A63 CRC64;

Query Match
Best Local Similarity 52.8%; Score 351; DB 11; Length 749;
Matches 64; Conservative 20; Mismatches 28; Indels 4; Gaps 2;

QY 1 GHEITHGFDNGRNFDRKNGNMWNSFSTQHFREQSECMYQYGNYSWDLADQNVNGF 60
Db 579 GHEITHGFDNGRKYDKANGNDLPWVSDESEKFEKTKCMYQYGNYSWYKXAG-LNVKRG 637
QY 61 NTLGENTADNGVRQAYKAYLKWMAEGGKDQQLPGLDLTHEOLFNFYNAQVWC 113
Db 638 RTLGENIADNGGLREAFRAYRKWINDRQGVVEPLPGITFTNNQLFSLTAHVRC 693

RESULT 13
O44857
ID O44857 PRELIMINARY; PRT; 750 AA.
AC O44857;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 87.0 KDA PROTEIN.
GN T05A8.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RA MEDLINE-99069613; PubMed-9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
```

RC STRAIN-BRISTOL N2;  
RA Wilson R., Henkhaus J., Wohldmann P.;  
RT "The sequence of C. elegans cosmid T05A8";  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Waterston R.;  
RT "Direct Submission";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF040652; AAB95021.1;  
DR HSSP: P08473; 1DWT.  
DR MEROPS: M13; UPW;  
DR InterPro: IPR000718; Peptidase\_M13.  
DR InterPro: IPR000130; Zn\_MTPetdase.  
DR Pfam: PF01431; Peptidase\_M13; 1.  
DR PRINTS: PR00786; NEPRILYSIN.  
DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 750 AA; 87021 MW; F87716C1B6450FE0 CRC64;

Query Match 52.4%; Score 348.5; DB 5; Length 750;  
Best Local Similarity 52.6%; Pred. No. 3.3e-27;  
Matches 60; Conservative 22; Mismatches 31; Indels 1; Gaps 1;  
QY 1 GHEITHGFDNGRNFDRKNGNMMDWNSFSTQHFREQSECMYIYQYNSWDLADEQNVNGF 60  
DB 584 GHEITHGFDNGRGLYDNLGNIRWMDNATISKFEKKAQCEKQYSSVLDQINMQ-INGK 642  
QY 61 NTLGENTADNGGVROAYKAYLKWAEGGKDOQLPGLDLTHEOLFINTYAOVWCCK 114  
DB 643 STRGENTADNGGLKQAYRAYKYEKRSRPRPLGVNLTHDLPFLYAOIWCCK 696

## RESULT 14

Q96NX3 PRELIMINARY; PRT; 736 AA.  
AC Q96NX3  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE ENDOTHELIN CONVERTING ENZYME-2B.  
GN ECE2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lorenzo M.-N., Khan R.Y., Wang Y., Tai S.C., Chan G.C., Cheung A.H.,  
RA Marsden P.A.;  
RT "Human endothelin converting enzyme-2 (ECE2): characterization of mRNA  
species and chromosomal localization."  
RL Biochim. Biophys. Acta 0:0-0(2002).  
DR EMBL: AF428264; AAL30387.1;  
SQ SEQUENCE 736 AA; 83322 MW; 77F14FE5AC80E187 CRC64;

Query Match 51.7%; Score 343.5; DB 4; Length 736;  
Best Local Similarity 50.9%; Pred. No. 1e-26;  
Matches 59; Conservative 18; Mismatches 36; Indels 3; Gaps 1;  
QY 1 GHEITHGFDNGRNFDRKNGNMMDWNSFSTQHFREQSECMYIYQYNSWDLADEQNVNGF 60  
DB 572 GHEITHAFDDQGREYDKGNLRPWQNESLAARHNTACMEEQYNOYQ---VNGERLNGR 628  
QY 61 NTLGENTADNGGVROAYKAYLKWAEGGKDOQLPGLDLTHEOLFINTYAOVWCCK 116  
DB 629 QTLGENTADNGGLKAAAYKAYKAWLRKHGEEQOLPAVGLTNHOLFVGFVGAQWCVSR 684

## RESULT 15

Q96NX4 PRELIMINARY; PRT; 787 AA.  
AC Q96NX4  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE ENDOTHELIN CONVERTING ENZYME-2A.  
GN ECE2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lorenzo M.-N., Khan R.Y., Wang Y., Tai S.C., Chan G.C., Cheung A.H.,  
RA Marsden P.A.;  
RT "Human endothelin converting enzyme-2 (ECE2): characterization of mRNA  
species and chromosomal localization."  
RL Biochim. Biophys. Acta 0:0-0(2002).  
DR EMBL: AF428263; AAL30386.1;  
SQ SEQUENCE 787 AA; 89221 MW; CC2D2B0F0EBF7239 CRC64;  
Query Match 51.7%; Score 343.5; DB 4; Length 787;  
Best Local Similarity 50.9%; Pred. No. 1.1e-26;  
Matches 59; Conservative 18; Mismatches 36; Indels 3; Gaps 1;  
QY 1 GHEITHGFDNGRNFDRKNGNMMDWNSFSTQHFREQSECMYIYQYNSWDLADEQNVNGF 60  
DB 623 GHEITHAFDDQGREYDKGNLRPWQNESLAARHNTACMEEQYNOYQ---VNGERLNGR 679  
QY 61 NTLGENTADNGGVROAYKAYLKWAEGGKDOQLPGLDLTHEOLFINTYAOVWCCK 116  
DB 680 QTLGENTADNGGLKAAAYKAYKAWLRKHGEEQOLPAVGLTNHOLFVGFVGAQWCVSR 735  
Search completed: October 3, 2002, 11:07:02  
Job time: 95 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2002, 11:05:27 ; Search time 16.05 Seconds  
(without alignments)  
694,477 Million cell updates/sec.

Title: US-09-647-780A-4  
Perfect score: 665  
Sequence: 1 GHEITHGFDDNGRNFKNKN.....DLTHEQLFFINYAQVWCGCK 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description         |
|------------|-------|-------------|--------|----------|---------------------|
| 1          | 578   | 86.9        | 774    | 2 JC7265 | neprilysin (EC 3.4  |
| 2          | 469   | 70.5        | 750    | 1 HYHUN  | neprilysin (EC 3.4  |
| 3          | 489   | 70.5        | 751    | 1 HYHUN  | neprilysin (EC 3.4  |
| 4          | 485   | 69.9        | 750    | 1 HYHUN  | neprilysin (EC 3.4  |
| 5          | 374.5 | 56.3        | 754    | 2 S47268 | endothelin-conver   |
| 6          | 370.5 | 55.7        | 754    | 2 A53679 | endothelin-conver   |
| 7          | 370.5 | 55.7        | 758    | 2 A54667 | endothelin-conver   |
| 8          | 367.5 | 55.3        | 758    | 2 JC2521 | endothelin-conver   |
| 9          | 367.5 | 55.3        | 770    | 2 JC4136 | endothelin-conver   |
| 10         | 348.5 | 52.4        | 750    | 2 D88082 | protein T05A8.4 [i  |
| 11         | 341.5 | 51.4        | 766    | 2 T20003 | hypothetical prote  |
| 12         | 339.5 | 51.1        | 825    | 2 I46078 | endothelin-conver   |
| 13         | 338   | 50.8        | 590    | 2 C88099 | protein Fl8A12.8 [  |
| 14         | 263   | 39.5        | 769    | 2 T24949 | hypothetical prote  |
| 15         | 257   | 38.6        | 754    | 2 T16182 | hypothetical prote  |
| 16         | 253   | 38.0        | 1389   | 2 T22668 | hypothetical prote  |
| 17         | 223.5 | 33.6        | 700    | 2 B82788 | metalloproteinase X |
| 18         | 218.5 | 32.9        | 667    | 2 C87236 | probable zinc meta  |
| 19         | 215.5 | 32.4        | 798    | 2 T28906 | hypothetical prote  |
| 20         | 205   | 30.8        | 823    | 2 T28132 | hypothetical prote  |
| 21         | 202.5 | 30.5        | 706    | 2 F87683 | peptidase M13 fami  |
| 22         | 201.5 | 30.3        | 663    | 2 C70838 | probable zinc meta  |
| 23         | 179   | 26.9        | 630    | 2 F95191 | endopeptidase O [i  |
| 24         | 179   | 26.9        | 630    | 2 C98058 | endopeptidase O (E  |
| 25         | 165   | 24.8        | 627    | 2 C86850 | neutral endopeptid  |
| 26         | 165   | 24.8        | 627    | 2 A47098 | lactococcal endope  |
| 27         | 163   | 24.8        | 627    | 2 F53290 | endopeptidase Pepo  |
| 28         | 163.5 | 24.6        | 564    | 2 T11548 | probable zinc meta  |
| 29         | 163   | 24.5        | 534    | 2 T32020 | hypothetical prote  |

protein Fl8A12.1 [ ]  
hypothetical prote  
protein Fl8A12.4 [ ]  
protein Fl8A12.3 [ ]  
kell blood group p  
protein Fl8A12.6 [ ]  
hypothetical prote  
hypothetical prote  
hyaluronate lyase  
hypothetical prote  
chitinase homolog  
large repetitive p  
uncharacterized pr  
zinc metalloprotei  
hypothetical prote  
hypothetical prote

## ALIGNMENTS

## RESULT 1

JC7265

neprilysin (EC 3.4.24.11) II - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 02-Sep-2000

C:Accession: JC7265

R:Janja, O.; Facchinetti, P.; Rose, C.; Bonhomme, M.C.; Gros, C.; Schwartz, J.C.

Biochem. Biophys. Res. Commun. 271, 565-570, 2000

A:Title: Neprilysin II: A putative novel metalloprotease and its isoforms in CNS and

A:Reference number: JC7265

A:Contents: Brain and testis

A:Accession: JC7265

A:Molecule type: mRNA

A:Residues: 1-774 <TAN>

C:Genetics:

A:Gene: nepII

C:Superfamily: neprilysin

C:Keywords: brain; glycoprotein; hydrolase; metalloproteinase; neuropeptide; testis;

Query Match 86.9%; Score 578; DB 2; Length 774;

Best Local Similarity 85.1%; Pred. No. 7.5e-48;

Matches 97; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GHEITHGFDDNGRNFKNKNMMDWMSNFSTQHFQSECMYQYGNYSWDLADEQNNGF 60

Db 607 GHEITHGFDDNGRNFKNKNMMDWMSNFSAHFQSQCMYQYGNYSWELADNQNVNGF 666

Qy 61 NTLGENIADNGVRQAYKAYLKWMAEGKDOOLPGLDLTHEOLFFINYAQVWCG 114

Db 667 STLGENIADNGVRQAYKAYLQWLAEGRDORLPGLNLTYAOLFFINYAQVWCG 720

## RESULT 2

HYHUN

neprilysin (EC 3.4.24.11) [validated] - human

N:Alternate names: Cbl0; common acute lymphocytic leukemia antigen; endopeptidase 24.

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 08-Dec-2000

C:Accession: A41387; A36173; S05275; J10084; S00350; S02228

Protein Data Bank: S00350; S02228; S05275; J10084; S00350; S02228

Protein Data Bank: S00350; S02228; S05275; J10084; S00350; S02228

Protein Data Bank: S00350; S02228; S05275; J10084; S00350; S02228

Protein Data Bank: S00350; S02228; S05275; J10084; S00350; S02228

A:Reference number: A41387; MUID: 89386688

A:Accession: A41387

A:Molecule type: DNA

A:Residues: 1-750 <DAA>

A:Cross-references: GB:M26605

Note: the authors translated the codon AAC for residues 14 and 72 as Asp.

Shipp, M.A.; Richardson, N.E.; Sayre, D.H.; Brown, N.R.; Masteller, E.L.; Clayton,

Protein Data Bank: S00350; S02228; S05275; J10084; S00350; S02228

A:Title: Molecular Cloning of the Common Acute Lymphoblastic Leukemia Antigen (CALLA)

A:Reference number: A36173; MUID:88263038

A:Accession: A36173

A:Molecule type: mRNA

A:Residues: 1-750 <SHI>

A:Cross-references: GB:J03779

A:Note: part of this sequence was confirmed by protein sequencing

R.Jongeneel, C.V.

submitted to the EMBL Data Library, August 1988

A:Reference number: S05275

A:Accession: S05275

A:Molecule type: mRNA

A:Residues: 1-750 <JON>

A:Cross-references: EMBL:Y00811; NID:g29625; PIDN:CAA68752.1; PID:g29626

J. Letarte, M.; Vera, S.; Tran, R.; Addis, J.B.L.; Onizuka, R.J.; Quackenbush, E.J.; Jong

R. Exp. Med. 168, 1247-1253, 1988

A:Title: Common active lymphocytic leukemia antigen is identical to neutral endopeptidase

A:Reference number: J0084; MUID:89010526

A:Accession: J0084

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 2-191; 211-737 <LET>

A:Cross-references: EMBL:Y00811

A:Note: part of this sequence, including the amino end of the mature protein, was confir

med by R. Malfroy, B.; Schofield, P.R.; Mason, A.J.; Schofield, P.R.

FEBS Lett. 229, 206-210, 1988

A:Title: Molecular cloning and amino acid sequence of human enkephalinase (neutral endop

A:Reference number: S00350; MUID:88152222

A:Accession: S00350

A:Molecule type: mRNA

A:Residues: 3-750 <MAL>

A:Cross-references: EMBL:X07166

A:Note: 467-Thr was also found

A:Comment: This enzyme inactivates a variety of peptide hormones, cleaving on the amino

new. A:Comment: This antigen is an important cell surface marker; glycoprotein in the diagnosi

C:Genetics:

A:Gene: GDB:MME

A:Cross-references: GDB:120190; OMIM:120520

A:Map position: 3q25.1-3q25.2

A:Introns: 54/1; 66/1; 120/1; 147/1; 179/1; 218/3; 240/3; 285/3; 319/3; 365/2; 396/3; 43

C:Superfamily: neprilysin

C:Keywords: glycoprotein; hydrolase; metalloproteinase; oligopeptidase; surface antigen;

F:2-750/Product: neprilysin #status experimental <MAT>

F:16-23/Region: stop-transfer sequence

F:29-51/Domain: transmembrane #status predicted <TMN>

F:52-750/Domain: extracellular #status predicted <EXT>

F:145,285,311,325,335,628/Binding site: carboxylate (Asn) (covalent) #status predicted

F:584,588/Binding site: zinc (His) #status predicted

F:585/Active site: Glu #status predicted

Query Match

Best Local Similarity 70.5%; Score 469; DB 1; Length 750;

Matches 76; Conservative 24; Mismatches 14; Indels 0; Gaps 0;

QY 1 GHEITHGDDNGRNFKNKGMMDWNSFSTQHFRQSECMYQYGNYSWDLADEQNVNGF 60

DB 583 GHEITHGDDNGRNFKNKGDLDVDMWTQSSANFKEQSCMVYQYGNFSDLAGGQHLNGI 642

QY 61 NTLGENIADNGGVQRAYKAYLKWMAEGGKDDQLPGLDLTHEOLFFINAYQVWCG 114

DB 643 NTLGENIADNGGLQAYRAYQNYIKKNGEKLPLGLDLNKHOLFLLNFAQVWCG 696

RESULT 3

HYRBN

N:Altrinate names: CD10; common acute lymphocytic leukemia antigen; endopeptidase 24.11;

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 18-Jun-1999

C:Accession: A29451; I46872

R:Devault, A.; Lazure, C.; Nault, C.; Le Moual, H.; Seidah, N.G.; Chretien, M.; Kahn, P.

EMBO J. 6, 1317-1322, 1987

A:Title: Amino acid sequence of rabbit kidney neutral endopeptidase 24.11 (enkephalin

A:Reference number: A29451; MUID:87275825

A:Accession: A29451

A:Molecule type: mRNA

A:Residues: 1-751 <DEV>

A:Cross-references: EMBL:X05338

A:Note: part of this sequence, including the amino end of the mature protein, was con

tributed to the EMBL Data Library, August 1988

A:Reference number: S05275

A:Accession: S05275

A:Molecule type: mRNA

A:Residues: 1-750 <JON>

A:Cross-references: EMBL:Y00811; NID:g29625; PIDN:CAA68752.1; PID:g29626

J. Letarte, M.; Vera, S.; Tran, R.; Addis, J.B.L.; Onizuka, R.J.; Quackenbush, E.J.; Jong

R. Exp. Med. 168, 1247-1253, 1988

A:Title: Common active lymphocytic leukemia antigen is identical to neutral endopeptidase

A:Reference number: J0084; MUID:89010526

A:Accession: J0084

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 2-191; 211-737 <LET>

A:Cross-references: EMBL:Y00811

A:Note: part of this sequence, including the amino end of the mature protein, was confir

med by R. Malfroy, B.; Schofield, P.R.; Mason, A.J.; Schofield, P.R.

FEBS Lett. 229, 206-210, 1988

A:Title: Molecular cloning and amino acid sequence of human enkephalinase (neutral endop

A:Reference number: S00350; MUID:88152222

A:Accession: S00350

A:Molecule type: mRNA

A:Residues: 3-750 <MAL>

A:Cross-references: EMBL:X07166

A:Note: 467-Thr was also found

A:Comment: This enzyme inactivates a variety of peptide hormones, cleaving on the ami

new. A:Comment: This antigen is an important cell surface marker; glycoprotein in the diagnosi

C:Genetics:

A:Gene: GDB:MME

A:Cross-references: GDB:120190; OMIM:120520

A:Map position: 3q25.1-3q25.2

A:Introns: 54/1; 66/1; 120/1; 147/1; 179/1; 218/3; 240/3; 285/3; 319/3; 365/2; 396/3; 43

C:Superfamily: neprilysin

C:Keywords: glycoprotein; hydrolase; metalloproteinase; oligopeptidase; surface antigen;

F:2-750/Product: neprilysin #status experimental <MAT>

F:16-23/Region: stop-transfer sequence

F:29-51/Domain: transmembrane #status predicted <TMN>

F:52-750/Domain: extracellular #status predicted <EXT>

F:145,285,311,325,335,628/Binding site: carboxylate (Asn) (covalent) #status predicted

F:584,588/Binding site: zinc (His) #status predicted

F:585/Active site: Glu #status predicted

Query Match

Best Local Similarity 70.5%; Score 469; DB 1; Length 751;

Matches 75; Conservative 25; Mismatches 14; Indels 0; Gaps 0;

QY 1 GHEITHGDDNGRNFKNKGMMDWNSFSTQHFRQSECMYQYGNYSWDLADEQNVNGF 60

DB 584 GHEITHGDDNGRNFKNKGDLDVDMWTQSSANFKEQSCMVYQYGNFSDLAGGQHLNGI 643

QY 61 NTLGENIADNGGVQRAYKAYLKWMAEGGKDDQLPGLDLTHEOLFFINAYQVWCG 114

DB 644 NTLGENIADNGGLQAYRAYQNYIKKNGEKLPLGLDLNKHOLFLLNFAQVWCG 697

RESULT 4

HYRBN

N:Altrinate names: CD10; common acute lymphocytic leukemia antigen; endopeptidase

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 18-Jun-1999

C:Accession: A29295; A33521

R:Malfroy, B.; Schofield, P.R.; Kuang, W.J.; Seeburg, P.H.; Mason, A.J.; Henzel, W.J.

Biochem. Biophys. Res. Commun. 144, 59-66, 1987

A:Title: Molecular cloning and amino acid sequence of rat enkephalinase.

A:Reference number: A29295; MUID:87213218

A:Accession: A29295

A:Molecule type: mRNA

A:Residues: 1-750 <MAL>

A:Cross-references: GB:M15944; NID:g204031; PIDN:AAA1116.1; PID:g204032

A:Note: part of this sequence, including the amino end of the mature protein, was con

R:Bateman Jr., R.C.; Jackson, D.; Slaughter, C.A.; Unnithan, S.; Chai, Y.G.; Moomaw,

J. Biol. Chem. 264, 6151-6157, 1989

A:Title: Identification of the active-site arginine in rat neutral endopeptidase 24.1

A:Reference number: A33521; MUID:89197908

A:Accession: A33521

A:Molecule type: protein

A:Residues: 95-102; 'X', 104-129 <BAT>

A:Comment: This enzyme inactivates a variety of peptide hormones, cleaving on the ami

new.

C:Superfamily: neprilysin

C:Keywords: glycoprotein; hydrolase; metalloproteinase; oligopeptidase; surface anti

F:9-750/Product: neprilysin #status experimental <MAT>

F:16-23/Region: stop-transfer sequence

F:29-51/Domain: transmembrane #status predicted <TMN>

```
F:52-750/Domain: extracellular #status predicted <EXT>
F:145,285,325,628/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:311/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:584,588/Binding site: zinc (His) #status predicted
F:585/active site: Glu #status predicted.
```

Query Match 69.9%; Score 465; DB 1; Length 750;  
Best Local Similarity 64.9%; Pred. No. 5.7e-37;  
Matches 74; Conservative 26; Mismatches 14; Indels 0; Gaps 0;

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| Qy | 1   | GHEITHGFDNDGRNFDKNGNMMDWNSFNSTQHFRSEQSECMYQYGNYSWDLADEQNNGVF | 60  |
|    |     | :     : ::: ::    :   :     :     : ::                       |     |
| Db | 583 | GHEITHGFDNDGRNFNKDGLVDWTQQSANFNFKDSOCMYQYGNTWDLAGGOHLNGI     | 642 |

Qy 61 NTLGENTADNGGVROAYKAYLKWMAEGKKDQLPGLDLTHEQLFFNYAQVWC 114  
| | | | | | | | : | | : : | | | | : | | | | : | | | |  
Db 643 NTLGENTADNGGIGQAYRAYQYVVKNGEKLPLGLDLNHKOLFFLNFQAQVWC 696

RESULT 5  
S47268  
endothelin-converting enzyme (EC 3.4.24.-) 1 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Oct-1999  
C:accession: S51010; S47268  
R:Schmidt, M.; Kroeger, B.; Jacob, E.; Seulberger, H.; Subkowski, T.; Otter  
FEBS Lett. 356, 238-243, 1994  
A:Title: Molecular characterization of human and bovine endothelin converti  
A:Reference number: S51009; MUID:95104423

A: Accession: S31010  
A: Status: preliminary  
A: Molecule type: mRNA  
A: Residues: 1-754 <SC2>  
A: Cross-references: EMBL:Z35306; NID:G535074; PIDN:CAA84547.1; PID:G535075  
C: Superfamily: neprilysin  
C: Keywords: hydrolase; metalloproteinase; zinc  
F: 591.595/Binding site: zinc, catalytic (His) #status predicted  
F: 592/Active site: Glu #status predicted

Query Match 56.3%; Score 374.5; DB 2; Length 754;  
Best Local Similarity 54.3%; Pred. No. 3e-28;  
Matches 63; Conservative 23; Mismatches 27; Indels 3; Gaps 1;

```

QY 1 GHEITHGDDNGRNFDKNGNMMDWNSFNSTOHFREQSECMYGYGNSWDLADEONVNGF 60
 IIIII III III III III III III III III III III III III III III
Db 590 GELTHAFDDOGRYDKOGNLRPPWKNSSVFAFKOOTACMVEOYGNS---VNGRPVNGR 646

```

**Qy** 61 NTLGENIADNGVQRQAYKAYLKWMAEGGKDQQLPLGLDTHQEUFFINYAQVWCCK 116  
:|||||: :||| : : ||| : : ||| : : ||| :  
**Dd** 647 HTLGENIADNGLKAARYAYONVYKKNGAEOTLP TLGTNNOLFELSAFQVCVSVR 702

```

RESULT 6
A53679 endothelin converting enzyme (EC 3.4.24.-) - rat
C:Species: Rattus norvegicus (Norway Rat)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Jun-2000
C:Accession: A53679, J00189
R:Shimada, K.; Takahashi, M.; Tanzawa, K.
J. Biol. Chem. 269, 18275-18278, 1994
A:Title: Cloning and functional expression of endothelin-converting enzyme.
A:Reference number: A53679; MUID:94308046

```

A: Accession: A35679  
A: Status: preliminary  
A: Molecule type: mRNA  
A: Residues: 1-754 <SH1>  
A: Cross-references: GB:D29683; NID:Q529084; PIDN:BARA06152.1; PID:q529085  
C: Superfamily: neprilysin  
C: Keywords: glycoprotein; hydrolase; metalloproteinase; transmembrane protein; zinc  
F: 1-52/Domain: intracellular #status predicted <INT>  
F: 53-73/Domain: transmembrane #status predicted <TM>

F:74-754/Domain: extracellular #status predicted <EXT>  
F:129/Binding site: substrate (Arg) #status predicted  
F:150,171,194,254,300,346,367,523,616,635/Binding site: carbohydrate (Asn) (covalent)  
F:591,595/Binding site: zinc, catalytic (His) #status predicted  
F:592/Active site: Glu #status predicted

| Query Match           | Score | DB 2              | Length | 754        |
|-----------------------|-------|-------------------|--------|------------|
| Best Local Similarity | 55.7% | 370.5             | DB 2   | Length 754 |
| Matches               | 54.3% | Pred. NO. 7.4e-28 |        |            |
| Conservative          | 63    | Mismatches        | 21     | Indels     |
|                       |       |                   |        | Gaps       |
|                       |       |                   |        | 1:         |

QY 1 GHEITHGFDNCRNFDCNGNMDDWNSFSTQHFRQSECMIIYYGYNSWDLADEQNVEF 60  
|||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

Dd 590 GHETHAFDGOGREYDKDGNLRPWKNKSVEAFKOOTECMVQOYNYS---VNGEPVNGR 648

QY      61    NTLGENTADNGVRQAYKAYLKWMAEGGKDQOLPGLDLTHEQLFTINYAQVWCCK    116  
         :| | | | | | | | | | :| | | | | . : : : | | | | | :| | | | | :| | | | |  
D8      647   HTLGENTADNGGUKAAYRAYONWVKNGAEOTIPTIGLTNOLFRTGFAOVMSVR    702

RESULT 7  
A54667  
endothelin converting enzyme (EC 3.4.24.-) 1 - bovine  
C.Species: Bos primigenius taurus (cattle)  
C.Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 05-Nov-1999  
C.Accession: A54667; JC2448  
R.Xu, D.; Emoto, N.; Giald, A.; Slaughter, C.; Raw, S.; dewit, D.; Yanagisawa,  
Cell 78, 473-485, 1994  
A.Title: EC5-1: a membrane-bound metalloprotease that catalyzes the proteolytic  
A.Reference number: A54667; MUID:94340737

A:Accession: A54667  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-758 <XUA>  
A:Cross-references: GB:U27342; NID:9897601; PID:AAA82928.1; PID:9897602.  
R:Kura, T.; Sawamura, T.; Shiraki, T.; Hosokawa, H.; Kido, T.; Hoshikawa, H.; Shimada  
Biochem. Biophys. Res. Commun. 203, 1417-1422, 1994  
A:Title: cDNA cloning and expression of bovine endothelin converting enzyme.  
A:Reference number: JG2448. MIMD-95032010.

A.Molecule type: mRNA  
A.Residues: 1-90,'A',92-698,'A',700-758 <IKU>  
A.Cross-references: G3:S73774; NID:9588289; PIDN:AA832063.1; PID:5688290  
C.Superfamily: neprilysin

C:keywords: hydrolase; metalloproteinase; transmembrane protein; zinc  
F:57-77/Domain: transmembrane #status predicted <TM>  
F:595,599/Binding site: zinc, catalytic (His) #status predicted  
F:596/Active site: Glu #status predicted

|                       |       |             |       |      |        |     |
|-----------------------|-------|-------------|-------|------|--------|-----|
| Query Match           | 55.7% | Score       | 370.5 | DB 2 | Length | 758 |
| Best Local Similarity | 53.4% | Best No. of | 48-28 |      |        |     |

QY 1 GHEITHGDDNRNFDKNGNMMDWSNFSTQHFRQSECMYQYGYSWDLADEQNNGF 60  
||||| |||| | : ||| : ||| : ||| : ||| : ||| : |||  
db CUEI MUA FOC DEVCACNT NNYXICUUTSFCZOMSGUCRGTGOWG 65

61 NTLGENIADNGVRQAYKAYLKWMAEGGKDQQLPGLDITHEQLFFINYAQVWCGCK 116

RESULT 8  
JC2521  
endothelin converting enzyme (EC 3.4.24.-).1, umbilical vein endothelial cell form  
C:Species: Homo sapiens (man)  
C:Date: 17-May-1995 #sequence\_revision 14-Jul-1995 #text\_change 20-Jun-2000  
C:Accession: JC2521  
R:Shimada, K.; Matsushita, Y.; Wakabayashi, K.; Takahashi, M.; Matsubara, A.; Iijima,  
Biochem. Biophys. Res. Commun. 207, 807-812, 1995  
A:Title: Cloning and functional expression of human endothelin-converting enzyme cDNA  
Reference number: JC2521: MUID: 95169128

Query Match 55.3%; Score 367.5; DB 2; Length 770;  
Best Local Similarity 53.4%; Pred. No. 1.5e-27;  
Matches 62; Conservative 21; Mismatches 30; Indels 3; Gaps 1;

submitted to the EMBL Data Library, March 1996

A:Reference number: Z20417

A:Accession: T27775

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-766 cW12>

A:Cross-references: EMBL:Z69904; PIDN:CAA93782.1; GSPDB:GN00020; CESP:ZK20.6

A:Experimental source: clone ZK20

C:Genetics:

A:Gene: CESP:ZK20.6

A:Map position: 2

A:Introns: 11/1; 334/3; 439/1; 692/3; 734/2





